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SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Wright, David A.  
Voytas, Daniel F.

<120> Plant Retroelements and Methods Related Thereto

<130> P-1065A

<140> 09/586,106

<141> 2000-06-02

<150> 60/087,125

<151> 1998-05-29

<150> 09/322,478

<151> 1999-05-28

<160> 190

<170> PatentIn Ver. 4.0

<210> 1

<211> 18

<212> DNA

<213> Glycine max

<400> 1

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18

<210> 2

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<212> DNA

<213> Glycine max

<400> 2

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<210> 3

<211> 6

<212> DNA

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<400> 3

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6

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<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

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<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 5

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atccttccag agaggaatgt agagcttgga ccagggatgt ttgatgagtt cctgcaggaa 180
ctccagaggc tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt 240
gctctggtga aggagtttta ctccaaccta tatgatccag aggaccacag tccgaagttt 300
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360
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cctccagacc atgatgccat cctttccgct ctgtgtactc cagggggacg atttgttctg 480
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tga 1263
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<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 6

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1 5 10 15

Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr  
20 25 30

Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu

35					40					45					
Leu	Gly	Pro	Gly	Met	Phe	Asp	Glu	Phe	Leu	Gln	Glu	Leu	Gln	Arg	Leu
50						55					60				
Arg	Trp	Asp	Gln	Val	Leu	Thr	Arg	Leu	Pro	Glu	Lys	Trp	Ile	Asp	Val
65					70					75					80
Ala	Leu	Val	Lys	Glu	Phe	Tyr	Ser	Asn	Leu	Tyr	Asp	Pro	Glu	Asp	His
				85					90					95	
Ser	Pro	Lys	Phe	Trp	Ser	Val	Arg	Gly	Gln	Val	Val	Arg	Phe	Asp	Ala
			100					105					110		
Glu	Thr	Ile	Asn	Asp	Phe	Leu	Asp	Thr	Pro	Val	Ile	Leu	Ala	Glu	Gly
			115				120					125			
Glu	Asp	Tyr	Pro	Ala	Tyr	Ser	Gln	Tyr	Leu	Ser	Thr	Pro	Pro	Asp	His
	130					135					140				
Asp	Ala	Ile	Leu	Ser	Ala	Leu	Cys	Thr	Pro	Gly	Gly	Arg	Phe	Val	Leu
145					150					155					160
Asn	Val	Asp	Ser	Ala	Pro	Trp	Lys	Leu	Leu	Arg	Lys	Asp	Leu	Met	Thr
				165				170						175	
Leu	Ala	Gln	Thr	Trp	Ser	Val	Leu	Ser	Tyr	Phe	Asn	Leu	Ala	Leu	Thr
			180					185					190		
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Leu	Val	Met	Lys	Met	Asp	Leu	Asp	Val	Gly	Ser	Leu	Ile	Ser	Leu	Gln
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Ile	Ser	Gln	Ile	Ala	Gln	Ser	Ile	Thr	Ser	Arg	Leu	Gly	Phe	Pro	Ala
225					230					235					240
Leu	Ile	Thr	Thr	Leu	Cys	Glu	Ile	Gln	Gly	Val	Val	Ser	Asp	Thr	Leu
				245					250					255	
Ile	Phe	Glu	Ser	Leu	Ser	Pro	Val	Ile	Asn	Leu	Ala	Tyr	Ile	Lys	Lys
			260					265					270		
Asn	Cys	Trp	Asn	Pro	Ala	Asp	Pro	Ser	Ile	Thr	Phe	Gln	Gly	Thr	Arg
	275						280					285			
Arg	Thr	Arg	Thr	Arg	Ala	Ser	Ala	Ser	Ala	Ser	Glu	Ala	Pro	Leu	Pro
	290					295					300				
Ser	Gln	His	Pro	Ser	Gln	Pro	Phe	Ser	Gln	Arg	Pro	Arg	Pro	Pro	Leu
305					310					315					320
Leu	Ser	Thr	Ser	Ala	Pro	Pro	Tyr	Met	His	Gly	Gln	Met	Leu	Arg	Ser
				325					330					335	
Leu	Tyr	Gln	Gly	Gln	Gln	Ile	Ile	Ile	Gln	Asn	Leu	Tyr	Arg	Leu	Ser

340

345

350

Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg  
 355 360 365

Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu  
 370 375 380

Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp  
 385 390 395 400

Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu  
 405 410 415

Gly Arg Gly Ser Glx  
 420

&lt;210&gt; 7

&lt;211&gt; 1596

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: plant  
 retroelement sequence

&lt;400&gt; 7

atgCGaggta gaactgcatc tggagacgtt gttcctatta acttagaaat tgaagctacg 60  
 tgTCggcgta acaacgctgc aagaagaaga agggagcaag acatagaagg aagtagttac 120  
 acctcacctc ctcttctctc aaattatgct cagatggacg gggaaccggc acaaagagtc 180  
 acactagagg acttctctaa taccaccact ctcagttct ttacaagtat cacaaggccg 240  
 gaagtccaag cagatctcct tactcaaggg aacctcttcc atggctcttcc aaatgaagat 300  
 ccataatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt 360  
 ccaaaagatg cgatactcct taacctcttt tcttttccc tagcaggaga ggcaaaaaga 420  
 tgggtgcact cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480  
 ttaaaagaagt atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatattc 540  
 catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga 600  
 aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660  
 caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720  
 atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat 780  
 gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaaac 840  
 aagctgttga cgaggcagat agaagccctc atcgaaaccc tcagcaagct gcctcaacaa 900  
 ttacaagcga taagtctctc ccactcttct gttttgcagg tagaagaatg ccccatatgc 960  
 agagggacac atgagcctgg acaatgtgca agccaacaag accctctctg tgaagtaaatt 1020  
 tatataggca tactaaatcg ttacggattt cagggtaca accagggaat tccatctgga 1080  
 ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac 1140  
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 ccaccatacc agccaccata ccagcacctc agccaaggtc cgaatcagca agaaaaagccc 1260  
 accaaaatag aggaactgct gctgcaattc atcaaggaga caagatcaca tcaaaaagagc 1320  
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 gaacggccca ctagaacttt cgggtgctaac atggagagaa gaaccccaag gaaggataaa 1440  
 gcagtactga ctagagggca gagaagagcg caggaggagg gtaagggttg aggagaagac 1500  
 tggccagaag aaggaaggac agagaagaca gaagaagaag agaaggtggc agaagaacct 1560  
 aagcgtacca agagccagag agcaaggga gccaaag 1596



<210> 8  
 <211> 532  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 8  
 Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu  
 1 5 10 15  
 Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu  
 20 25 30  
 Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn  
 35 40 45  
 Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp  
 50 55 60  
 Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro  
 65 70 75 80  
 Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu  
 85 90 95  
 Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys  
 100 105 110  
 Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn  
 115 120 125  
 Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser  
 130 135 140  
 Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe  
 145 150 155 160  
 Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu  
 165 170 175  
 Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu  
 180 185 190  
 Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser  
 195 200 205  
 Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile  
 210 215 220  
 Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala  
 225 230 235 240  
 Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His  
 245 250 255

Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr  
 260 265 270  
 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu  
 275 280 285  
 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile  
 290 295 300  
 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys  
 305 310 315 320  
 Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser  
 325 330 335  
 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly  
 340 345 350  
 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe  
 355 360 365  
 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly  
 370 375 380  
 Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln  
 385 390 395 400  
 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln  
 405 410 415  
 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys  
 420 425 430  
 Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu  
 435 440 445  
 Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr  
 450 455 460  
 Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys  
 465 470 475 480  
 Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val  
 485 490 495  
 Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu  
 500 505 510  
 Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala  
 515 520 525  
 Arg Glu Ala Lys  
 530

<211> 603  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 9  
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 atcatggaag tagagatctt tgactgttgg ggcatagact tcatggggcc ttttccttcg 120  
 tcatacggga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc 180  
 atagccacgc caaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt 240  
 tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat 300  
 cagttgaaga aagtccctgga gcactataat gtccgacata aggtggccac accttatcac 360  
 cctcagacaa atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaaag 420  
 acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480  
 aggacagcgt tcaagactcc catcggtcta tcaccatttc agctagtgtg tgggaaggca 540  
 tgtcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600  
 gac 603

<210> 10  
 <211> 201  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 10  
 Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met  
 1 5 10 15  
 Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile  
 20 25 30  
 Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu  
 35 40 45  
 Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro  
 50 55 60  
 Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe  
 65 70 75 80  
 Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His  
 85 90 95  
 Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg  
 100 105 110  
 His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu  
 115 120 125  
 Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser

130 135 140

Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr  
 145 150 155 160

Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val  
 165 170 175

Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr  
 180 185 190

Trp Ala Leu Lys Leu Leu Asn Phe Asp  
 195 200

<210> 11  
 <211> 600  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 11  
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 gttccaaga aaggtggaat gacagtggta cgagatgaga ggaatgactt gataccaaca 120  
 cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180  
 aaggaccatt tccccttacc ttcatggat cagatgctgg agagacttgc agggcaggca 240  
 tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300  
 caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360  
 gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg 420  
 gtggagaaaa gcatcgaggt atttatggac gacttctcgg ttttggacc ctcatttgac 480  
 agctgtttga ggaacctaga gagggactt cagaggtgcg aagagactaa cttggtactg 540  
 aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca 600

<210> 12  
 <211> 200  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 12  
 Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser  
 1 5 10 15

Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp  
 20 25 30

Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met  
 35 40 45

Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe

50	55	60
Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala		
65	70	75 80
Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val		
	85	90 95
Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val		
	100	105 110
Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr		
	115	120 125
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser		
	130	135 140
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp		
145	150	155 160
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr		
	165	170 175
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly		
	180	185 190
Ile Val Leu Gly His Lys Ile Ser		
	195	200

<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 13

aaggaagaac	cactagccct	tccacaggat	ctcccatatc	ctatggcacc	caccaagaag	60
aacaaggagc	gttactttgc	acgtttcttg	gaaatattca	aagggttaga	aatcactatg	120
ccattcgggg	aagcettaca	gcagatgccc	ctctactcca	aatttatgaa	agacatcctc	180
accaagaagg	ggaagtatat	tgacaacgag	aatattgtgg	taggaggcaa	ttgcagtgcg	240
ataatacaaa	ggattctacc	caagaagttt	aaagaccccc	gaagtgttac	catcccgtgc	300
accattggga	aggaagccgt	aaacaaggcc	ctcattgatc	taggagcaag	tatcaatctg	360
atgcccttgt	caatgtgcaa	aagaattggg	aatttgaaga	tagatcccac	caagatgacg	420
cttcaactgg	cagaccgctc	aatcacaagg	ccatatgggg	tggtagaaga	tgtcctggtc	480
aaggtacgcc	acttcacttt	tccggtggac	tttgttatca	tggatatcga	agaagacact	540
gagattcccc	ttatcttagg	cagacccttc	atgctgactg	ccaactgtgt	ggtggatatg	600
gggaaaggga	acttagagtt	gactattgat	aatcagaaga	tcacctttga	ccttatcaag	660
gcaatgaagt	acccacagga	gggttggaag	tgcttcagaa	tagaggagat	tgatgaggaa	720
gactgtcagtt	ttctcgagac	accaaagact	tcgctagaaa	aagcaatggt	aaatcattta	780
gactgtctaa	ccagtgaaga	ggaagaagat	ctgaaggctt	gcttggaaaa	cttggatcaa	840
gaagacagta	ttcctgag					858

<210> 14  
 <211> 286  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 14  
 Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala  
 1 5 10 15  
 Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile  
 20 25 30  
 Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln  
 35 40 45  
 Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly  
 50 55 60  
 Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala  
 65 70 75 80  
 Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val  
 85 90 95  
 Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile  
 100 105 110  
 Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg  
 115 120 125  
 Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala  
 130 135 140  
 Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val  
 145 150 155 160  
 Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile  
 165 170 175  
 Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu  
 180 185 190  
 Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr  
 195 200 205  
 Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr  
 210 215 220  
 Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu  
 225 230 235 240  
 Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met  
 245 250 255

Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys  
260 265 270

Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu  
275 280 285

<210> 15  
<211> 192  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 15  
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gacaaggtat ttcacgccat ctattatgct agcaaggtcc tgaatgaagc acagttgaat 120  
tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcagggtca 180  
tacttgatag gg 192

<210> 16  
<211> 64  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 16  
Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Leu  
1 5 10 15

Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys  
20 25 30

Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met  
35 40 45

Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly  
50 55 60

<210> 17  
<211> 12286  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant

## retroelement sequence

&lt;400&gt; 17

tgataactgc	taaataattg	tgaattaata	gtagaaaatt	agtcaaattt	tggtctaaaa	60
ttaattat	agcagttatt	tgtgattaaa	agttagaaaa	gcaattaagt	tgaatttttg	120
gccatagata	tgaaaactga	aggtacaaca	agcaaaaggc	agcagaaagt	gaagaaaaag	180
aataaaatct	gaagcagacc	cagcccaaca	cgcgccctta	gcgcgcgtca	cgcgctaagc	240
ttgcaaggca	gcacaggcac	taagcgaggc	gttaagcacg	aagatgcagg	attcggttacg	300
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Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro  
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Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu  
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Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys  
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Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn  
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<211> 1857

<212> DNA

<213> *Arabidopsis thaliana*

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<210> 25

<211> 1254

<212> DNA

<213> *Pisum sativum*

<400> 25

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<210> 26

<211> 564

<212> DNA

<213> Arabidopsis thaliana

<400> 26

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<210> 27

<211> 180

<212> DNA

<213> Arabidopsis thaliana

<400> 27

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<210> 28

<211> 192

<212> DNA

<213> Arabidopsis thaliana

<400> 28

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<210> 29  
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 <212> DNA  
 <213> Pisum sativum

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<210> 30  
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<210> 31  
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 <212> DNA  
 <213> Pisum sativum

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 <212> DNA

<213> Glycine max

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<210> 33

<211> 192

<212> DNA

<213> Glycine max

<400> 33

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tatttggtag gc 192
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<210> 34

<211> 597

<212> DNA

<213> Glycine max

<400> 34

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<210> 36  
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 <213> Glycine max

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<400> 37  
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<210> 38  
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<400> 38  
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<210> 39  
 <211> 27  
 <212> DNA  
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<400> 39  
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<210> 41  
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<210> 42  
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 <213> Nicotiana tabacum

<400> 42  
 gtgcgtaaag aggttttttaa actggagatt atcaagtgat tggatgccgg gggttatctac 60  
 cccattttacg atagtctcatg aacttctccg gtgcaatgtg tcccaaagaa ggtggcatga 120  
 cgggtggtcac caatgagaag aatgagttga ttcctacaag aatggtgacc ggttggagag 180  
 tgtgcatgga ctatcgcaag ctcaacaaac tcacaaggaa ggatcatttc ccatttccat 240  
 tccttgacca aatgcttgat aggttggcat gtcgtgcttt ctattgcttt ctagatgtat 300  
 agtcgggcta tagccaaatc tttattgctc cgtaggatca cgagaaaata cctttacatg 360  
 tccctatggg acttttgcct acaagcggat gccatttggg ttgtgtaatg cactagcgaa 420  
 cttttatagg tgtatgatgg ctatcttcac ggacatgggt aaggactacc ttaaagtgtt 480  
 catggatgac ttctcgatgg ttggggattc ctttgatgat tgcttggaata atttggataa 540  
 agtattggca agatatgaag aaacgaattt ggtactaaat tgggagaagt gtcatttcat 600  
 gatcgaggaa ggcattgttc ttggccacaa gatctcaaat aatggcattg aagtcgacaa 660  
 ggcaaagatt aaggtgattt ctaaacttac acctccaact ttggtgaaaag gcgtgcggag 720  
 tttcttaggc cacgcgggggt tttaccaatt cttcataaaa gatttcacaa aggtt 775

<210> 43  
 <211> 259  
 <212> PRT  
 <213> Nicotiana tabacum

<400> 43  
 Val Arg Lys Glu Val Phe Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala  
     1                    5                    10                    15  
 Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln  
                     20                    25                    30  
 Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn  
                     35                    40                    45  
 Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp  
                     50                    55                    60

Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro  
 65 70 75 80  
 Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys  
 85 90 95  
 Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx  
 100 105 110  
 Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr  
 115 120 125  
 Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg  
 130 135 140  
 Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val  
 145 150 155 160  
 Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu  
 165 170 175  
 Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val  
 180 185 190  
 Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu  
 195 200 205  
 Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile  
 210 215 220  
 Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg  
 225 230 235 240  
 Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe  
 245 250 255

Thr Lys Val

<210> 44

<211> 761

<212> DNA

<213> *Nicotiana tabacum*

<400> 44

gtgcgtaaag aggtggtcaa gctgttggat gtcgggggttg tgtaccccat ctctgatagc 60  
 tcttggactt cgccggtgca atgtgtacca aagaagggtt gcatgactgt ggtgaaaaat 120  
 tccaaaaatg agttgattcc gacaagaacc atcaccggtt ggagggtatg catggactac 180  
 cgcaagttga ataaagtgac ctgcaaggat cactttcctt tgccatttct ggatcagatg 240  
 ctatgacgac ttgctgggagc tgccttctat tgcttcttgg atgaatattc tgggtataac 300  
 caaatcttga ttgctccgga agatccggaa aagaccacat tcacttgtcc gtatggcaca 360  
 tttgttttct ctaggatgcc ttttaggttg tgtaatgcac cagctacatt tcagcggtgt 420  
 atgatggcca ttttctccta tatggtgaaa gacatttttg aggtgttcat ggacgatttt 480  
 agtgttgtgg ggcactcatt tgatgaatgc ttgaagaatc ttgatagggt gttggcccat 540  
 tgtgaagaaa ccaatcttgt cctcaattgg gagaaatgcc actttatggt agaagaagga 600

atcaatctctt ggcataaaat ttcaaaacat ggcattgagg tggataaaca aagatagatg 660  
 tgatttcaag gctccctccc cctacatccg tcaaggaggt ccgatgtttt cttgggcatg 720  
 cggggttcta ttggagattc ataaaagact tctccaaggt t 761

<210> 45  
 <211> 254  
 <212> PRT  
 <213> Nicotiana tabacum

<400> 45  
 Val Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro  
 1 5 10 15  
 Ile Ser Asp Ser Ser Trp Thr Ser Pro Val Gln Cys Val Pro Lys Lys  
 20 25 30  
 Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr  
 35 40 45  
 Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met  
 65 70 75 80  
 Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr  
 85 90 95  
 Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe  
 115 120 125  
 Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140  
 Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg  
 165 170 175  
 Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser  
 195 200 205  
 Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg  
 210 215 220  
 Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val

<210> 46  
 <211> 762  
 <212> DNA  
 <213> *Nicotiana tabacum*

<400> 46  
 gtgcgtaagg aggtgtttta gttgttgat gttgggggtg tgtaccccat ctctgatagc 60  
 tcttgcatTT cgcgggtgca atgtgtaccg aagaagggtg gcatgaccgt ggttgcaaT 120  
 tcgcaaaatg gggttgattcc taccaggatc gtcaccgggt ggaagggtatg catggattac 180  
 cgaaagttga ataaagtga cgcgaaggat cactttccat tgccttttct tgatcagatg 240  
 ttagatcgac ttgctgggCG tgccttctac tgtttcttgg atgggtattc tggatacaac 300  
 caaatcttca ttactccgga agatcaggag aagacaacat tcacttgTcc atatggcacc 360  
 tttgcttttt ctaggatgcc ttttgggttg tgtaatgcac cgactacatt ctagcggtat 420  
 atgatggcca ttttactga tatggtggaa gatattttgg aggtgttcat ggacgacttt 480  
 agtgttgtgg gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540  
 tgtaaagaaa ccaatcttgt tcttaattgg gagaaatgcc acttcatggt tgaggaggggc 600  
 atagtTcttg ggcataaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgat 660  
 gtgatttcaa ggctccctcc ccctacttct gtcaagggtg tgagaagttt tcttaggcat 720  
 gcgggggttct accggagatt catcaaagat ttcaccaaag tt 762

<210> 47  
 <211> 254  
 <212> PRT  
 <213> *Nicotiana tabacum*

<400> 47  
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro  
 1 5 10 15  
 Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr  
 35 40 45  
 Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met  
 65 70 75 80  
 Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Tyr Asn Gln Ile Phe Ile Thr Pro Glu Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Ser Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Tyr Met Met Ala Ile  
 130 135 140



Phe Thr Asp Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Val Gly Asp Ser Phe Asp Glu Cys Leu Asn Asn Leu Asp Arg  
 165 170 175  
 Val Leu Ala His Cys Lys Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Glu Glu Gly Ile Val Leu Gly His Lys Ile Leu  
 195 200 205  
 Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg  
 210 215 220  
 Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Arg His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 48  
 <211> 760  
 <212> DNA  
 <213> Nicotiana tabacum

<400> 48  
 gcggaaggag gtcgtcaagc tgttgatgt cggtgtgtg taccocatat ttgatagctc 60  
 ttggactttg ccggtgcaat atgtgccgaa gaagggtggt atgaccgtgg ttaccaatgt 120  
 aaaaaatgag ttgattccta ccaggactgt caccgggtgg aggggtgtgca tggattacca 180  
 caaattgaat aaagtgaccc gcaaggatca ctttccatta ctttttcttg atcagatgtt 240  
 agacagactt gctgggtgtg ctttctactg tttcttggat gggattcttg ggtgcaacaa 300  
 aattttgatt gcacaaaaag atcaggagaa gaccaccttt actgtacgt atgggtacctt 360  
 tgtcttttct aggatgtcat ttgggtgtg taatgcaccg actacattct agaggtgtat 420  
 gatggccata tttacctaca tgggtggagga cattttggag gtgtttatgg atgacttcag 480  
 tgttgttggg gactagtttg atgaatgttt gaaaaatctt gatagagtgt tggcccgttg 540  
 tgaagaagcc aaccttgtgc ttaattggga gaaatgccac ttcattggtg aggagggtcat 600  
 agtccttagc cataaaattt caaagcatgg tatagaggtg gacaaagcaa aaattgaagt 660  
 gatttcaagg ctcttctccc ctacttctgt caaggaggtt agaagttttc ttgggcatgc 720  
 ggggttctac tggagattca tcaaagactt cacgaagggt 760

<210> 49  
 <211> 253  
 <212> PRT  
 <213> Nicotiana tabacum

<400> 49  
 Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro Ile  
 1 5 10 15  
 Phe Asp Ser Ser Trp Thr Leu Pro Val Gln Tyr Val Pro Lys Lys Gly  
 20 25 30  
 Gly Met Thr Val Val Thr Asn Val Lys Asn Glu Leu Ile Pro Thr Arg  
 35 40 45

Thr Val Thr Gly Trp Arg Val Cys Met Asp Tyr His Lys Leu Asn Lys  
 50 55 60  
 Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met Leu  
 65 70 75 80  
 Asp Arg Leu Ala Gly Cys Ala Phe Tyr Cys Phe Leu Asp Gly Tyr Ser  
 85 90 95  
 Gly Cys Asn Lys Ile Leu Ile Ala Pro Lys Asp Gln Glu Lys Thr Thr  
 100 105 110  
 Phe Thr Cys Thr Tyr Gly Thr Phe Val Phe Ser Arg Met Ser Phe Gly  
 115 120 125  
 Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Met Ala Ile Phe  
 130 135 140  
 Thr Tyr Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe Ser  
 145 150 155 160  
 Val Val Gly Asp Glx Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg Val  
 165 170 175  
 Leu Ala Arg Cys Glu Glu Ala Asn Leu Val Leu Asn Trp Glu Lys Cys  
 180 185 190  
 His Phe Met Val Glu Glu Gly Ile Val Leu Ser His Lys Ile Ser Lys  
 195 200 205  
 His Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Ser Arg Leu  
 210 215 220  
 Leu Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Gly His Ala  
 225 230 235 240  
 Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 50  
 <211> 762  
 <212> DNA  
 <213> Oryza sativa

<400> 50  
 gtgcgtaagg aggtgtttta gttcctgtat gccaggatta tttatctcgt accatacagc 60  
 gagtgggtta gccagttca ggtcgtgcca aagaaggag gaatgacggc cgttgcaaat 120  
 gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac 180  
 aggaaactta acaaggctac aaaaaaggat catttccgc tacccttcat tgatgaaatg 240  
 ttggaacggc tggcaaatca ttccttcttc tgtttccttg atgggtattc aggatatcat 300  
 caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360  
 tatgcgtatc gtaggatgcc ctttgactg tgcaacactc ctgcatcttt ccaaagggtg 420  
 atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc 480  
 tcggtctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaagt cttacaacga 540  
 tgccaagaaa aggacctagt gcttaactgg gaaaagtgcc atttcatggt ctgtgaaggg 600

atagttcttg ggcacgagt gtccgaacga ggagtcgaag ttgatcgtgc taaaattgat 660  
 gtgatagatc agcttcctcc acccgtgaac atcaaaggaa tccgcagctt ctttggtcac 720  
 gctggctttt atagaagggt catcaaggac ttcacaaaag tt 762

<210> 51  
 <211> 254  
 <212> PRT  
 <213> Oryza sativa

<400> 51  
 Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu  
   1                  5                  10                  15  
 Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
                   20                  25                  30  
 Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln  
           35                  40                  45  
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
       50                  55                  60  
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
       65                  70                  75                  80  
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
                   85                  90                  95  
 Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr  
           100                  105                  110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe  
       115                  120                  125  
 Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
       130                  135                  140  
 Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe  
       145                  150                  155                  160  
 Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys  
           165                  170                  175  
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys  
           180                  185                  190  
 Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser  
       195                  200                  205  
 Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln  
       210                  215                  220  
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His  
       225                  230                  235                  240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 52  
 <211> 761  
 <212> DNA  
 <213> *Oryza sativa*

<400> 52  
 gtgcgcaagg aggttttgaa attgctgcat gccaggatta tctatcccg accatacagt 60  
 gagagggtta gcccagtgcca ggttgtgcca aagaaggag gaatggcggt cgttgcaa 120  
 gctcagaatg aactaattac gcaacaaacc gtaaccgat ggaggatgtg tatcgattac 180  
 aggaaactca acaaggctac aaaaaaggat catttcccgc tacccttcat tgttgaaatg 240  
 ttggaacggc tggcaaatca ttccttcttt tgtttccttg atggatattt cggatatcat 300  
 caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc 360  
 tatgcgatc ataggatgtc ctttggactg tgcaacgctc ctgcatcttt ccaagggtga 420  
 tgatgtctat tttctcggac atgatcgagg atatcatgga agtcttcatg gatgacttct 480  
 cggctctatg aaagactttc ggtcattgtc tgcaaaatct agacaaagtc ttacaacgat 540  
 gccaaagaaa ggacctggtg ctttaactggg aaaagtgaca tttcatggtc cgtgaaggga 600  
 tagttcttgg gcatcgagtg ttcgaacaag gaatcgaagt tgatcatgct aaaattgatg 660  
 tgatagatca gcttctcct cccgtgaaca tcaaaggat ccgcagcttc ttgggtcatg 720  
 tcggctttta tagaagggtc atcaaggact tcactaaagt t 761

<210> 53  
 <211> 254  
 <212> PRT  
 <213> *Oryza sativa*

<400> 53  
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Arg Ile Ile Tyr Pro  
 1 5 10 15  
 Val Pro Tyr Ser Glu Arg Val Ser Pro Val Gln Val Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Ala Val Val Ala Asn Ala Gln Asn Glu Leu Ile Thr Gln  
 35 40 45  
 Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Val Glu Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Phe Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Glx Ser Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr His Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
 130 135 140

Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys  
 165 170 175  
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe  
 195 200 205  
 Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln  
 210 215 220  
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 54  
 <211> 762  
 <212> DNA  
 <213> Oryza sativa

<400> 54  
 gtgcggaag aggtttttaa gtcctgcat gccgggatta tttataccgt tccatgcagt 60  
 gagtgggtca gcacagtcca gggtgggccg aagatgggat gaatgacggt cgttgcaa 120  
 gctcaaaata aacttatccc gcaaccaacc ataaccgat ggaggatgtg catagactac 180  
 aggaaactca acaaggctac aaaagaggat cattttccgc tacccttcat tgatgaaatg 240  
 ttggaacgga tgacaaatca ttccttcttc tgtttccttg atgggtattc cggatatcat 300  
 caaattccca tccgtccaga ggaccagagt aagactacgt tcacatgtcc atatggcacc 360  
 tatgcgtatc gtaggatgtc ctccggactg tgcaacgctc ctgcatcttt ccaaagggtgt 420  
 atgttgtcta ttttctcgga catgatcgaa gatatcatga aagtcttcat ggatgacttc 480  
 tcagtttatg gaaagacttt cggtcattgt ctgtagaatc tagacaaagt cttacaacga 540  
 tgccaagaaa atgacctagt gtttaattgg gaaaagtgcc attttatggt ccgtgaaggg 600  
 atagtctctg ggcacgagt atccgaatga ggaatcgaag ttgatcgtgc taaaatcgat 660  
 gttatagatc aaattcgtcc tctgcgaat atcaaaggaa tccgcagctt cttgggacat 720  
 gccggctttt atagaaggtt cctcaaggac ttcacaaaag tt 762

<210> 55  
 <211> 254  
 <212> PRT  
 <213> Oryza sativa

<400> 55  
 Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Thr  
 1 5 10 15  
 Val Pro Cys Ser Glu Trp Val Ser Thr Val Gln Val Gly Pro Lys Met  
 20 25 30  
 Gly Glx Met Thr Val Val Ala Asn Ala Gln Asn Lys Leu Ile Pro Gln  
 35 40 45

Pro Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
 65 70 75 80  
 Leu Glu Arg Met Thr Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Tyr His Gln Ile Pro Ile Arg Pro Glu Asp Gln Ser Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Leu Ser Ile  
 130 135 140  
 Phe Ser Asp Met Ile Glu Asp Ile Met Lys Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Glx Asn Leu Asp Lys  
 165 170 175  
 Val Leu Gln Arg Cys Gln Glu Asn Asp Leu Val Phe Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Ser  
 195 200 205  
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln  
 210 215 220  
 Ile Arg Pro Pro Ala Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Leu Lys Asp Phe Thr Lys Val  
 245 250

<210> 56  
 <211> 762  
 <212> DNA  
 <213> *Oryza sativa*

<400> 56  
 gtgcgtaagg aggtcttgaa gctcttgcac gccgagatta tttatcccgt accatataga 60  
 gaggtagggtta gcccggtcta gggtatgccg aagaagggac gaatgacggt cattgcaaat 120  
 gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180  
 atgaaactta acaaggctac gaaaaaggat catttcccac tacccttcac tgatgaaatg 240  
 ttggaacggc tggcaaatca ttctttcttc cgtttccctg atgggtattc taggtatgat 300  
 caaattccca tccatccgga ggaccaaagt aagactacgt tcacatgttc gtatgatacc 360  
 tatgcttata gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaagggtg 420  
 atgatgtcta ttttctccga catgattaag gacattatgg aagtccttcac gcatgacttc 480  
 tctattttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat tttgcaacga 540  
 tgccaagaga aggacctggt acttaattgg gaaaagtgtc atttcatggt ccgtgaaggg 600

atagttcttta gtcacgaggt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660  
 gtaatagatt agcttccttc tcctgtgaac attaagggga tccgcaattt tttgggacat 720  
 gctggctttt atagaagggt catcaaagac ttcacaaagg tt 762

<210> 57  
 <211> 254  
 <212> PRT  
 <213> Oryza sativa

<400> 57  
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro  
 1 5 10 15  
 Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys  
 20 25 30  
 Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
 130 135 140  
 Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe  
 145 150 155 160  
 Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys  
 165 170 175  
 Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser  
 195 200 205  
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx  
 210 215 220  
 Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 58  
 <211> 762  
 <212> DNA  
 <213> Hordeum vulgare

<400> 58  
 gtgcgcaagg aggttttagaa gttcctggaa gcaggtatca tctatcgtgt tgctcatagt 60  
 gattgggtga gtcgggtgca ttgtgtccct aagaagggag gcattaccgt tgtccctaata 120  
 gataaggatg aattgatccc acagaggact attactggct ataggatggg gattgatttt 180  
 aggaaattga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaata 240  
 cgagaaaggc tgtctaaaca cacacacttc tgctttctaa acggttattt tggtttctcc 300  
 caaataccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttgggtaca 360  
 tttgcttata gacgtatgac ttttggctta tgtaatgcac ctgcctcctt tcaaagatgt 420  
 atgatggcta tattccctga cttttgtgaa aagattgttg aggttttcat ggatgacttc 480  
 tccatttacg gatcttcctt tgatgattgc ctcagcaacc ttgatcgagt cttgcagaga 540  
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggg taatgacggc 600  
 atcgtcttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taaggttgat 660  
 ggaatcgaga aaatgccata cccacagat atcaaaggga taagaagttt ccttggtcat 720  
 gctggtttct atagaagggt cataaaagac ttcactaagg tt 762

<210> 59  
 <211> 254  
 <212> PRT  
 <213> Hordeum vulgare

<400> 59  
 Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg  
 1 5 10 15  
 Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr  
 85 90 95  
 Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140



Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys  
 180 185 190  
 Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys  
 210 215 220  
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 60  
 <211> 762  
 <212> DNA  
 <213> Hordeum vulgare

<400> 60  
 gtgcgtaaag aggtcctaaa gttcctggaa gcgggtatta tctatcctgt tgctcacaac 60  
 gattgggtga gtccggtgca ttgcgtccct aagaaggat gcattaccgt tgtccctaata 120  
 gataaggatg aattgatccc acataggatt attactggct ataggatggg gatcgatttt 180  
 aggaaaatga ataaagccac taggaaagaa cattaccctt tgccttttag cgaccaaata 240  
 ctagaaagggt tgtctaaaca cacacacttc tgctttctag acggttattc tagtttctcc 300  
 caaatactag ttgcacaatc tgatcaggag aaaaccactt tcacctaccc gttcgggtacc 360  
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac ctgccacctt tcaaagatgt 420  
 atgatggcta tattctctga cttttgtgaa aagtttgcg aggttttcat ggatgacttt 480  
 tccgtttacg gatcttcctt tgatgattgc ctcaacaacc ttgatcgggt cttgcagaga 540  
 tgtaaagata ctaatcttgt cttgaattgg gagaagtgcc actttatggg taatgaaggc 600  
 atcgtcttag gacataaaat ttccgaaaga ggtattgaat tcgataaggc taagggttgg 660  
 gcaatcaaga aaatgccata cccacagat atcaaaggta taagaagttt cttggtccat 720  
 gctggtttct atagaagggt catcaaggac ttacaaaagg tt 762

<210> 61  
 <211> 254  
 <212> PRT  
 <213> Hordeum vulgare

<400> 61  
 Val Arg Lys Glu Val Leu Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Ala His Asn Asp Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Cys Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro His  
 35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Met Asn  
 50 55 60  
 Lys Ala Thr Arg Lys Glu His Tyr Pro Leu Pro Phe Ser Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Ser Phe Ser Gln Ile Leu Val Ala Gln Ser Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Tyr Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140  
 Phe Ser Asp Phe Cys Glu Lys Phe Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Asn Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Phe Asp Lys Ala Lys Val Gly Ala Ile Lys Lys  
 210 215 220  
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Val His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 62

<211> 757

<212> DNA

<213> Hordeum vulgare

<400> 62

gaaaagaggt tgtgaagctc ctggatgaag gtattatcta tcatgttgct catagcgatt 60  
 gggtagagtc ggtgcatagc gttcctaaga agggaggcat taccgttgct cctaatagata 120  
 aggatgaatt gatcccgagc aggattatca ctggctatag gatggtgatc gatttcagga 180  
 aactgaataa agccactagg aaagatcatt accctttgcc ttttatcgac catatgctag 240  
 aaaggttgtc caaactcaca cacttctgct ttctagacgg ttattctagt ttctcccaaa 300  
 taccagttgc acaatctgat caggagaaaa ccactttcac ctgccctttc ggtacctttg 360  
 cttatagacg tatgcctttt ggcttatgta atgcacctgc cacctttcaa agatgtatga 420  
 tggctatatt ctctaacttt tgtgaaaata ttgtcgaggt tttcatggat gacttttccg 480  
 ttacgggtc ttcttttgat gattgcctca gcaaccttga tcgagtctta cagagatgta 540  
 aagacaccaa tcttgtcttg aatggggaga agtgccactt tatggttaat gaaggcatcg 600

tcttaggaca taaaatttct gaaagaggta ttgaagtcga taaggctaag gttgatgcaa 660  
 tcgacaaaat gccatacccc acagatatca aaggtataag aagtttcctt ggtcatgggtg 720  
 gtttctatag aaggtttatc aaagatttca caaaggt 757

<210> 63  
 <211> 251  
 <212> PRT  
 <213> Hordeum vulgare

<400> 63  
 Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala  
 1 5 10 15  
 His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly  
 20 25 30  
 Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile  
 35 40 45  
 Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala  
 50 55 60  
 Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu  
 65 70 75 80  
 Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser  
 85 90 95  
 Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe  
 100 105 110  
 Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu  
 115 120 125  
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser  
 130 135 140  
 Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val  
 145 150 155 160  
 Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu  
 165 170 175  
 Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His  
 180 185 190  
 Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg  
 195 200 205  
 Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Asp Lys Met Pro  
 210 215 220  
 Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His Gly Gly  
 225 230 235 240  
 Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys

<210> 64  
 <211> 740  
 <212> DNA  
 <213> Hordeum vulgare

<400> 64  
 gtgcgtaaag aggtgattaa attcctagaa gaaggattta tctatcctgt tgcacacagc 60  
 gattgggtga gtccgggtgca ttgcattcct aagaaaggag gcattaccgt tgtccctaata 120  
 gataaggatg aattgatccc atagaggatt attactggct ataggatggg gattgatttt 180  
 aggaagtga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaagt 240  
 ctagaaaggc tgtctaaaca cacacacttc ttgtttctgg acggttatac tggtttctcc 300  
 caaataccag ttgcacaatt tgatcaggag aaaaccactt taacctgaca tttcgggtacc 360  
 tttgcttata tacgtatgcc ttttggcttg tgtaatgcac ctgccacctt tcaaagatgt 420  
 atgatggcta tattctccga cttctgtgaa aagattgtca atgttttcat ggataacttc 480  
 tccgtttacg ggtgttcctt tgatgattgc ctcaacaacg ttgatcgagt cttacagaga 540  
 tgtaaggaca ccaatgttg cttgaattgg gagaagtgtc actttatggg taatgaaggc 600  
 atcgtcttag gacataagat ttctgaaaga ggtattaaag ttgataaggc taaggttgat 660  
 gcaatcgaga aaatgccata tccacagata tcaaagggtat aagaagtttc cttgggtcatg 720  
 ctggtttcta tagaaggttc 740

<210> 65  
 <211> 247  
 <212> PRT  
 <213> Hordeum vulgare

<400> 65  
 Val Arg Lys Glu Val Ile Lys Phe Leu Glu Glu Gly Ile Ile Tyr Pro  
     1                    5                    10                    15  
 Val Ala His Ser Asp Trp Val Ser Pro Val His Cys Ile Pro Lys Lys  
                     20                    25                    30  
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Glx  
                     35                    40                    45  
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
     50                    55                    60  
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
     65                    70                    75                    80  
 Leu Glu Arg Leu Ser Lys His Thr His Phe Leu Phe Leu Asp Gly Tyr  
                     85                    90                    95  
 Thr Gly Phe Ser Gln Ile Pro Val Ala Gln Phe Asp Gln Glu Lys Thr  
                     100                    105                    110  
 Thr Leu Thr Glx His Phe Gly Thr Phe Ala Tyr Ile Arg Met Pro Phe  
     115                    120                    125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
     130                    135                    140

Phe Ser Asp Phe Cys Glu Lys Ile Val Asn Val Phe Met Asp Asn Phe  
 145 150 155 160  
 Ser Val Tyr Gly Cys Ser Phe Asp Asp Cys Leu Asn Asn Val Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Lys Asp Thr Asn Val Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Arg Gly Ile Lys Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220  
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe  
 245

<210> 66  
 <211> 762  
 <212> DNA  
 <213> Avena sativa

<400> 66  
 gtgcgaaagg aggttttcaa gctcatggat gctggtatta tttaccctat tgctgatagt 60  
 gaatgggtta gtcattgttca ttgtgttcct aaaaaggag gtattaccgt tgtccctaata 120  
 gataatgatg agcttattcc tcaaagaata gtggtaggct ataggatgtg catcgatttt 180  
 aggaaagtca ataaagtac taagaaagat cactaccgc ttccttttat tgatcaaagt 240  
 ttggaaagat tttctaaaaa gaccatttt tgttttcttg atggttattc tggtttctct 300  
 caaattgttg ttaaacaaca agatcaagaa aaaactactt ttacttgccc ttatggaact 360  
 tatgcttata gatgtatgcc ttttggttta tgtaatgtc cttctacttt cctaagggtgc 420  
 atgtctgcta tctttcatgg tttttgtgag gaaattgtag aagtgttcat ggacgacttt 480  
 tctgtctacg gaacttcttt tgataattgt ctgcacaacc ttgataaagt tttacagaga 540  
 tgtgaaggaa ctaattcttg tcttaattgg gagaaatgcc acttcatggt taatgaaggg 600  
 attgttcttg ggcataaagt ttctaaaaga ggcatagaag ttgatagagc taagggttgag 660  
 gcaattgaga agatgccatg tccaagagac atcaaaggta ttcgtagtat ccttggtcat 720  
 gctggtttct ataggagggt catcaaagac ttcacaaagg tt 762

<210> 67  
 <211> 254  
 <212> PRT  
 <213> Avena sativa

<400> 67  
 Val Arg Lys Glu Val Phe Lys Leu Met Asp Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Ile Ala Asp Ser Glu Trp Val Ser His Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln  
 35 40 45

Arg Ile Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn  
 50 55 60  
 Lys Val Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Phe Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Phe Ser Gln Ile Val Val Lys Gln Gln Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Cys Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ser Thr Phe Leu Arg Cys Met Ser Ala Ile  
 130 135 140  
 Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys  
 165 170 175  
 Val Leu Gln Arg Cys Glu Gly Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Lys Arg Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys  
 210 215 220  
 Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 68  
 <211> 762  
 <212> DNA  
 <213> Avena sativa

<400> 68  
 gtgcgcaaaag aggtcttttaa gttccttgat gctgggtatta tttaccctat tgctgatagt 60  
 caatgggtta gccttggttca ttgtgtcccc aagaaagggg gaataactgt tgtgcctaata 120  
 gaagataatg agcttatacc ccaaagagta gtggttggtg atagaatgtg cattgatattt 180  
 agaaggatta ataaagttac taggaaagat cattatcctt tgccctttat tgatcaaatg 240  
 cttgagaggt tgtccaaaaa gactcacttt tgttttcttg atgggtcattc tgggttttct 300  
 caaattgttg tgaaagcaca agaccaagag aaaactactt tcaattgtcc ttatggtact 360  
 tatgattata ggcgtatgcc ttttggttta tgtaatgctc ctgctacctt tcagagatgt 420  
 atgtctgcta tatttcatgg tttttgtgaa gaaattgtgg aggttttcat ggacgatttt 480  
 tctgtctatg gaacttcttt tgataactgt ttgcacaacc ttgataaatt tttgcagaga 540  
 tttgaagaaa ccaaccttgt tcttaattgg gagaaatgcc atttcatggg taatgaaggg 600

attgttcttg gacacaagat ctcagaaaga ggcattgaag ttgacagagc caaaattgaa 660  
gcaattgaga acatgccttg ccctagagat attaaaggta ttcgtagtat ccttggtcat 720  
gctgggttct atagtaggtt catcaaagac tttacaaaag tt 762

<210> 69  
<211> 254  
<212> PRT  
<213> Avena sativa

<400> 69  
Val Arg Lys Glu Val Phe Lys Phe Leu Asp Ala Gly Ile Ile Tyr Pro  
1 5 10 15  
Ile Ala Asp Ser Gln Trp Val Ser Leu Val His Cys Val Pro Lys Lys  
20 25 30  
Gly Gly Ile Thr Val Val Pro Asn Glu Asp Asn Glu Leu Ile Pro Gln  
35 40 45  
Arg Val Val Val Val Tyr Arg Met Cys Ile Asp Phe Arg Arg Ile Asn  
50 55 60  
Lys Val Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80  
Leu Glu Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly His  
85 90 95  
Ser Gly Phe Ser Gln Ile Val Val Lys Ala Gln Asp Gln Glu Lys Thr  
100 105 110  
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Asp Tyr Arg Arg Met Pro Phe  
115 120 125  
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile  
130 135 140  
Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160  
Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys  
165 170 175  
Phe Leu Gln Arg Phe Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190  
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
195 200 205  
Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Ala Ile Glu Asn  
210 215 220  
Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His  
225 230 235 240  
Ala Gly Phe Tyr Ser Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 70  
 <211> 756  
 <212> DNA  
 <213> Avena sativa

<400> 70  
 aaggagggttt ttaaactcct tgatgttggt attatattacc ctattgctga tagtgaatgg 60  
 gttagtcttg ttcattgtgt tcctaaaaag ggaggtatta ccgttggtcc taatgataat 120  
 gatgagctta ttcctcaaag aatagtggta ggctatagga tgtgcataga ttttaggaaa 180  
 gttaataaag ttactaagaa agatcactac ccgcttcctt ttattgatca aatgttggaa 240  
 aggttggtcta aaaagaccca tttttgtttt cttgatgggtt actctagctt ctctcaaatt 300  
 gctgtttaaac aacaagatca agaaaaaact acttttactt gcccttatgg aacttttgct 360  
 tatagacgta tgcctattgg tttatgtaat gctcctgcta cttttcaaag gtgtatgtct 420  
 gctatatctt atggtttttg tgaggaaaatt gtagaagtgt tcatggatga cttttctgtc 480  
 tatggaactt cttttgataa ttgcctgcac aaccttgata aagttttgca gagatgtgaa 540  
 gaaactaata ttgttcttaa ttgggagaaa ttccacttca tggttaatga agggattgtc 600  
 cttgggcata aagtttctaa aagaggcata gaagttgata gagctaaggt tgaggcaatt 660  
 gagaagatgc catgcccaag agacatcaaaa ggtatacgta gtatccttgg tcatgctggt 720  
 ttctatagaa ggtttatcaa agacttcaca aagggtt 756

<210> 71  
 <211> 252  
 <212> PRT  
 <213> Avena sativa

<400> 71  
 Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro Ile Ala  
 1 5 10 15  
 Asp Ser Glu Trp Val Ser Leu Val His Cys Val Pro Lys Lys Gly Gly  
 20 25 30  
 Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln Arg Ile  
 35 40 45  
 Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn Lys Val  
 50 55 60  
 Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met Leu Glu  
 65 70 75 80  
 Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser  
 85 90 95  
 Phe Ser Gln Ile Ala Val Lys Gln Gln Asp Gln Glu Lys Thr Thr Phe  
 100 105 110  
 Thr Cys Pro Tyr Gly Thr Phe Ala Tyr Arg Arg Met Pro Ile Gly Leu  
 115 120 125  
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile Phe His  
 130 135 140



Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe Ser Val  
 145 150 155 160

Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys Val Leu  
 165 170 175

Gln Arg Cys Glu Glu Thr Asn Ile Val Leu Asn Trp Glu Lys Phe His  
 180 185 190

Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser Lys Arg  
 195 200 205

Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys Met Pro  
 210 215 220

Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His Ala Gly  
 225 230 235 240

Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 72

<211> 748

<212> DNA

<213> Secale cereale

<400> 72

gtgcggaaaag aggtctttaaa actcctagag gcagggtatta actatcccat tgctgatagc 60  
 cagcggggttaa gtcattgtcca ttgtgttcct aagaaaggag gtatgactgt cgtccctaag 120  
 gataaagatg aatttatccc gcaaagaata gttacagggt ataggatggt aattgatttt 180  
 cgtaagttaa ataaagctac tatgaaagat cattaccct tgccatttat tgatcaaatg 240  
 ccagacagggt tatccaaaca tactcatttc tgctttctag atggttattc tgggtttctct 300  
 caaatacctt tgtcaaaggg ggatcaagaa aagaccacct ttacttggtcc tttcgggtacc 360  
 tttgcttata gaggtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420  
 atgatcggtta tattctctgt cttttttgaa aagattgttg aggtattcat ggatgatttc 480  
 tccgtttatg gaacttcttt tgatgattgc ttaagcaacc ttgatcgagt tttgcagaga 540  
 tgtgaagata ctaaccttgt cttgaattgg gagaagtgcc actttatggt taatgaaggc 600  
 attttcttgg gacataaaat ttctgaaaga ggtactgaag ttgagaaagc taaagtggat 660  
 gctattgaaa agatgccatg ccctaaggat atgaaaggta tacgaagttt ccttggtcac 720  
 gctgggtttt ataggagggt cataaaag 748

<210> 73

<211> 249

<212> PRT

<213> Secale cereale

<400> 73

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Asn Tyr Pro  
 1 5 10 15

Ile Ala Asp Ser Gln Arg Val Ser His Val His Cys Val Pro Lys Lys  
 20 25 30

Gly Gly Met Thr Val Val Pro Lys Asp Lys Asp Glu Phe Ile Pro Gln  
 35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Met Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Pro Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Phe Ser Gln Ile Pro Leu Ser Lys Gly Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Gly Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ile Val Ile  
 130 135 140  
 Phe Ser Val Phe Phe Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Phe Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Arg Gly Thr Glu Val Glu Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220  
 Met Pro Cys Pro Lys Asp Met Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys  
 245

<210> 74

<211> 762

<212> DNA

<213> Secale cereale

<400> 74

gtgcggaagg aggtcgttaa gcttccagag gcaggtatta tctatcccgt tgctgatagc 60  
 cagtgggttaa gtcattgtcca ttgtgtccct aagaaggagg gtatgactgt cgttcctaatt 120  
 gacaaacatg aattgatccc gcaaagaata gttacagggt ataggatgggt aattgatttc 180  
 cgtaagttaa ataaagctac taagaaagat cattaccctt tgccatttat tgatcaaattg 240  
 ctagacaggt tatccaaaca tactcatttt tgctttctag atggttatta tggtttctct 300  
 caaataacctg tgtcaaaaagg ggatcaagaa aagaccactt tcacttgctc tttcggtacc 360  
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac ctgctacctt tcaaagatgt 420  
 atgatggcta tattatctga tttttgagaa aagattgttg aggttttcat ggatgatttc 480  
 tccggttacg gaacttcttt tgatgactac ttaagcaaca atgatcgagt tttgcagaga 540  
 tgtgaagaca ctaatcttgt tttgaattgg gagaagtgcc actttatggt taatgaaggc 600

attgtcttgg gacaaaaaat ttctgaaaga ggtattgaag ttgacaaagc taaagtcgat 660  
gctgttgaaa agatgccatg cccaaggac atcaaaggta tacgaagttt ccttggtcat 720  
gttgggtttt ataggagggtt catcaaagac ttcacgaaag tt 762

<210> 75  
<211> 254  
<212> PRT  
<213> Secale cereale

<400> 75  
Val Arg Lys Glu Val Val Lys Leu Pro Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15  
Val Ala Asp Ser Gln Trp Val Ser His Val His Cys Val Pro Lys Lys  
20 25 30  
Gly Gly Met Thr Val Val Pro Asn Asp Lys His Glu Leu Ile Pro Gln  
35 40 45  
Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
50 55 60  
Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
65 70 75 80  
Leu Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
85 90 95  
Tyr Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr  
100 105 110  
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125  
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
130 135 140  
Leu Ser Asp Phe Glx Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
145 150 155 160  
Ser Val Tyr Gly Thr Ser Phe Asp Asp Tyr Leu Ser Asn Asn Asp Arg  
165 170 175  
Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190  
Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly Gln Lys Ile Ser  
195 200 205  
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys  
210 215 220  
Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240  
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 76  
 <211> 762  
 <212> DNA  
 <213> Secale cereale

<400> 76  
 gtgcgtaagg aggtgggttaa gctcctagaa gcagggtatta tctatccagt tgctgatagt 60  
 cagtgggttaa gtcattgtcca ttatgttcct aagaaaggag gtatgactgt tgtccctaata 120  
 gataaagatg aattgatccc gcaaagaata gttacagggt ataggatggt aagtgatttc 180  
 cgtaagttga ataaagccac taagaaagat cattaccctc tgccatttat tgatcaaatg 240  
 ctagaaagggt tatccaaaca tactcatttc ttctttctag atggttattc tgggtttctc 300  
 caaataccctg tgtcaaaagg ggatcaagaa aagaccacct ttacttgtag tttcgggtacc 360  
 tttgcttata gacgtatgcc ttttgggttta tgtaatgcac ctgctacctt tcaaagatgc 420  
 atgatgggcta tattctctga cttttgtgaa aagattgttg aggtattcat ggatgatttc 480  
 tccgttttacg gaacttcctt tgatgattgc ttaagcaacc ttgatcgagt tttgcagaga 540  
 tgtgaagaca ctaaccttgt cttgaattgc gagaagtgcc actttatggt taatgaaggc 600  
 attgtcttgg gacataaaat ttctgaaata ggtattgaag ttgacaaagc taaagttgat 660  
 gctattgaaa agatgccatg cgcaaaggac atcaaaggta tacggagttt ccttggtcat 720  
 gccgggtttt ataggagggt catcaaagat ttctcaaagg tt 762

<210> 77  
 <211> 254  
 <212> PRT  
 <213> Secale cereale

<400> 77  
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Ala Asp Ser Gln Trp Val Ser His Val His Tyr Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Ile Val Thr Gly Tyr Arg Met Val Ser Asp Phe Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ser Lys His Thr His Phe Phe Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Phe Ser Gln Ile Pro Val Ser Lys Gly Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Thr Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Asp Thr Asn Leu Val Leu Asn Cys Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Ile Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220  
 Met Pro Cys Ala Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 78  
 <211> 759  
 <212> DNA  
 <213> Secale cereale

<400> 78  
 gtgcgcaagg aagtttttaa gtttctagag gcaggtataa tctatccagt tgctgatagc 60  
 cagtgggtaa gtcctgtcca ttgtgtccct aagaaggag gtatgactgt agttccta 120  
 gataaagatg aattgatctc gcaaagaatt gttacagggt ataggatggg aattgatttt 180  
 cgcaaattaa ataaagccac taagaaagat caataccctt tgccttttat tgatcaaagt 240  
 ctagaaagggt tatccaaaca caccattttt tgctttctag atgggtattc tagtttctct 300  
 caaataccta tgtcaaaagg ggataaagaa aagaccactt ttacttgtcc ctttgggtact 360  
 ttgcttatag acgtatgcct tttggtttat gtaatgcatc tgctaccctt caaacatgca 420  
 tgatgggctat actctatgat ttttgtgaaa gaatgttgat gttttcatgg atgatttttg 480  
 tattttacgaa acttcttttg atgattgctt gagcaacctt gatcgagttt tgcagagatg 540  
 tgaagaaact aatcttgtct tgaactggga aaagtccac tttatgggta atgaaggcat 600  
 tgcttgggac ataaaatttc tgaaagaggt accgaagtg acaaagctaa agttgatgct 660  
 gttgaaaaga tgccatgtcc caaggacatc aaagggtataa gaagtttcct tggatcatgcc 720  
 gggttttata ggaggtttat caaggacttc accaagggtt 759

<210> 79  
 <211> 254  
 <212> PRT  
 <213> Secale cereale

<400> 79  
 Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Ser Gln  
 35 40 45

Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Lys Asp Gln Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Ser Phe Ser Gln Ile Pro Met Ser Lys Gly Asp Lys Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Ser Ala Thr Phe Gln Thr Cys Met Met Ala Ile  
 130 135 140  
 Leu Tyr Asp Phe Cys Glu Arg Ile Val Asp Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Cys Ile Tyr Glu Thr Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Ser His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Arg Gly Thr Glu Val Asp Lys Ala Lys Val Asp Ala Val Glu Lys  
 210 215 220  
 Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 80  
 <211> 761  
 <212> DNA  
 <213> Triticum aestivum

<400> 80  
 gtgcgtaagg aggttctcaa gtttctggag gtaggtataa tttatcccg tgcgtgatagt 60  
 cagtgggtaaa gtctctgtcca ttgtgtccct aagaagggag gtattactgt tgtccctaata 120  
 gataaagatg aattgattcc tcaaagaatt attacgggta taggatggta attgatttcc 180  
 gcaaattaaa taaagccact aagagagatc attaccctt accttttatt gatcaaattc 240  
 tagaaagatt atgcaaacat acacattatt gcttccaaga tggttatcct ggtttttctc 300  
 aaatacctgt gtcggctaaa gatcaatcaa agactacttt tacatgccct tttggtactt 360  
 ttgcttatag atgtatgcct tttggtttat gtaatgcacc tgctaccctt caaagatgca 420  
 tgatggctat attctctgat ttttggtgaaa agatttgatg ggttttcatg gatgactttt 480  
 ccgtctatgg ttctctttt gatgattgct tgagcaatct tgatcgagtt ttgcagagat 540  
 gtgaagaaac taatcttgtc ttgaattggg aaaagtgtca ctttatgggt aatgaaggta 600

ttgtcttggg gcacaaagtt tctgaaagag gtattgaagt tgataaagcc aaggttgaca 660  
 ctattgaaaa gataccatgt cccaaggaca tcaaagggtac aagaagtttc cttgggtcacg 720  
 ccggatttta taggagggttc ataaaagatt tcacaaaggt t 761

<210> 81  
 <211> 254  
 <212> PRT  
 <213> Triticum aestivum

<400> 81  
 Val Arg Lys Glu Val Leu Lys Phe Leu Glu Val Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Ala Asp Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Arg Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Ile  
 65 70 75 80  
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Gln Asp Gly Tyr  
 85 90 95  
 Pro Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140  
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Thr Ile Glu Lys  
 210 215 220  
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Thr Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

<210> 82  
 <211> 780  
 <212> DNA  
 <213> Triticum aestivum

<400> 82  
 gtgcggaagg aggtgtttta gctccttgag gcagggtataa tttatcccgt tgctgatagt 60  
 aagtggggtaa ttcctgtcca ttaagtgatc gtgattactg ttgttcctaa gaagggaggt 120  
 attaccgttg ttcctaataa taaagatgaa ttgattcctc aaagaacccat tactgggttat 180  
 aggatggtaa ttgatttccg caaattaaat aaggctacta aaaaatatca ttaccocctta 240  
 ccttttatcg atcaaagtct agaaagatta tccaaacata cacatttttg ctttctagat 300  
 ggttactctg gtttctctca aatacctgtg tcagccaaag atcaatcaaa gactactttt 360  
 acatgccctt ttgggtacttt tgcttataga cgtatgcctt ttgggttatg taatgcacct 420  
 gctacctttc aaagatacat gatggctata ttatctgact tttgtgaaaa gatttgtgag 480  
 gttttcatgg acgactcttc catctatgga tcttcttttg atgattgctt gagcaacctt 540  
 gatcgagttt tgcagagatg tgaagaaact tatcttgtct tgaattggga aaagtgccaa 600  
 tttatggtta atgaaggatg tgcctggggg cataaagttt ctgaaagagg tattcgagtt 660  
 gataaagcca aggttgatgc tattgaaaag atgccatgct ccatggacat caaagggtata 720  
 agaagtttcc ttggtcatgc cggtttttat aggaggttca taaaagactt cacgaagggt 780

<210> 83  
 <211> 260  
 <212> PRT  
 <213> Triticum aestivum

<400> 83  
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Ala Asp Ser Lys Trp Val Ile Pro Val His Glx Val Ile Val Ile  
 20 25 30  
 Thr Val Val Pro Lys Lys Gly Gly Ile Thr Val Val Pro Asn Asp Lys  
 35 40 45  
 Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile  
 50 55 60  
 Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu  
 65 70 75 80  
 Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe  
 85 90 95  
 Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala  
 100 105 110  
 Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala  
 115 120 125  
 Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln  
 130 135 140



Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu  
145 150 155 160

Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys  
165 170 175

Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu  
180 185 190

Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val  
195 200 205

Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys  
210 215 220

Val Asp Ala Ile Glu Lys Met Pro Cys Pro Met Asp Ile Lys Gly Ile  
225 230 235 240

Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp  
245 250 255

Phe Thr Lys Val  
260

<210> 84  
<211> 762  
<212> DNA  
<213> Triticum aestivum

<400> 84  
gtgcgtaagg aggtattcaa gcttctggag gcagggtataa tttatcccgt tgttgatagt 60  
caatgggtaa gtccgtgtcca ttgtgtcctt aagaagggag gtattactgt tgtccctaata 120  
gataaagatg aattgattcc gcaaagaatt atcacagggt ataggatggg aattgatttc 180  
cgtaagttaa ataaagctac taagaaagat cattaccctt taccttttat tgatcaaatg 240  
ttagaaagat tatgcaaaca tacacattat tgctttctag atggttattc tggtttctct 300  
caaatacctg tgtcagctaa ggatcaatca aagactactt ttacatgccc ttttgggtact 360  
tttgggtata gacgtatgcc tttcgattta tgtaatgcac ctgctacctt tcaaatatgc 420  
atgatggcta tattctctga cttttgcgaa aagatttgtg aggttttcat ggacgacttt 480  
tccgtctatg gttcctctta tgatgattgc ttgagcaatc ttaatcgagt tttgcagaga 540  
tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggg taatgaagggt 600  
attgtcttgg ggcacaaaagt ttctgaacga ggtattgaag ttgataaggc caagggtgat 660  
gctattgaaa agatgacatg tcccaaggac atcaaaggta taagaagttt ccttggtcac 720  
gccagatttt ataggagggt cataaaagac ttcacaaagg tt 762

<210> 85  
<211> 254  
<212> PRT  
<213> Triticum aestivum

<400> 85  
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Val Asp Ser Gln Trp Val Ser Pro Val His Cys Val Leu Lys Lys  
20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
           35                          40                          45  
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
           50                          55                          60  
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
           65                          70                          75                          80  
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr  
                           85                          90                          95  
 Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr  
                           100                          105                          110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Gly Tyr Arg Arg Met Pro Phe  
           115                          120                          125  
 Asp Leu Cys Asn Ala Pro Ala Thr Phe Gln Ile Cys Met Met Ala Ile  
           130                          135                          140  
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Asp Phe  
           145                          150                          155                          160  
 Ser Val Tyr Gly Ser Ser Tyr Asp Asp Cys Leu Ser Asn Leu Asn Arg  
                           165                          170                          175  
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
                           180                          185                          190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
           195                          200                          205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
           210                          215                          220  
 Met Thr Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
           225                          230                          235                          240  
 Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
                           245                          250

<210> 86

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 86

gtgcggaaag aggtgctcaa gcttctggag gcaggataaa tttatcccgt tgctgagagt 60  
 cagtgggttaa gtccgtgcca ttgtgtccct aagaagggag gtattactgt tgtccctaata 120  
 gataaagatg aattgattcc tcaaagaatt attacagggt ataggatggt aattgatttc 180  
 cgcaaattaa ataaagccac caagaaagat cattaccctt taccttttat tgatcaaatg 240  
 ctgaaaagat tatgcaaaca tacacattat tgcttcctag atgggtattc tgggtttctct 300  
 caaataacctg tgcgggctaa agatcaatca aagactactt ttacatgccc ttttggtact 360  
 tttgcttata gacgtatgcc ttttggttta tgtaatgcac cttctacctt tcaaagatgc 420

atgatggcta tattctctga tttttgtgaa aagatttgtg aggttttcat ggacgaattt 480  
 tccgtctatg gttcctcttt tgatgattgc ttgagcaatc ctgatcgagt tttgcagaga 540  
 tgtgaagaaa ctaatcttgt cttgaattgg gaaaagtgcc actttatggg taatgaaggt 600  
 attgtcttgg ggcacaaaagt ttctgaaaga ggtattgaag ttgataaagc caagggttgac 660  
 gctattgaaa agatgccatg tccaaggac atcaaaggta taagaagttt ccttggtcac 720  
 gccggatttt ataggagggt cataaaaagac ttcacaaaagg tt 762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro  
 1 5 10 15

Val Ala Glu Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys  
 20 25 30

Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln  
 35 40 45

Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn  
 50 55 60

Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80

Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr  
 100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125

Gly Leu Cys Asn Ala Pro Ser Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140

Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Glu Phe  
 145 150 155 160

Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Pro Asp Arg  
 165 170 175

Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190

Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220

Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His

225

230

235

240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

&lt;210&gt; 88

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Triticum aestivum

&lt;400&gt; 88

gtgcgtaagg aggttttcaa gttccttgag gcagggtatta cttatcccgt tgctgatagt 60  
 gaatgggtaa gccctctcca ttgtgttcct aaaaagggag gtattaccgt tggtcttaaat 120  
 gataaagatg aattgatccc gcaaataatt attacagggt ataggatggg aattgatttc 180  
 cataagttaa ataaagctac taagaaagat cattaccctt tacctcttat tgatcaaat 240  
 ctgaaaagac tatccaaaca cacacatttc tgctttctag atgggtatac tgggtttctct 300  
 caaataacctg tgtcagtgaa ggatcaatct aaaactactt ttacttgccc ttttggtact 360  
 tttgcttata gacttatgcc ttttggttta tgtaatgcac ctacttcctt tcaaagatgc 420  
 atgatggcta tattctctgt tttttgtgaa aatatttgtg aggtattcat ggatgatttc 480  
 tccgtttatg gatcctcttt tgatgattgt ttgagcaacc ttgatcgagt tttgcagaga 540  
 tgcaagaca ctagtctcat cctgaattgg gaaaagtgtc actttatggg taatgaaggc 600  
 attgtcttgg ggcataagat ttccgagaga ggtattgaag ttgacaaagc caaagttgat 660  
 gctattgaaa agattccatg tcccaaggac ataaaaggta taagaagttt ccttggtcat 720  
 gctgggtttt ataggagggt catcaaagac ttctcaaagg tt 762

&lt;210&gt; 89

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 89

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro  
 1 5 10 15  
 Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln  
 35 40 45  
 Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile  
 65 70 75 80  
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe  
 115 120 125

Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140  
 Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys  
 210 215 220  
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 90  
 <211> 791  
 <212> DNA  
 <213> *Gossypium hirsutum*

<400> 90  
 gtgcgcaagg aggttttaaa gctacttgat gacgggatga tctatcccat atctaacagt 60  
 aattgggtta gcccagtaca catagtacca aaaaagacca gtgcaaccgt aatcgagaat 120  
 tcggcaggtg agatagttcc cactcgggtc caaaacgggt ggagagtatg catcgattac 180  
 aggaagttga attccttaac tcggaaggat cactttccac ttctttttat tgaccagatg 240  
 ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300  
 tgtgttttgg atggttacta aggttttttc cagatcccag tggcaccgga ggatcaagaa 360  
 agacaatgtt tacgtgcccc tttggcacgt tttcttacag acggatgccg ttcggactct 420  
 gtaatgcacc agccagtttt cataggtgca tggtaagtat attttcagac tacgtcgata 480  
 aaattatcga ggtgttcatt gacgacttta ctgtatatgg tgagtccttc gaggtaagtc 540  
 tgacgaacct tgcaaaaatt ttggaaagat gcttagaatt taatcttggt ctaaattatg 600  
 agaaatgcc a ttttatggta gacaagggat tagttctagg tcatattatt tctgctgatg 660  
 gaatttctgt tgataaagca aaaatcaaca tcattaactc actaccatac cccacaactg 720  
 tgagggagat ttggtctttc cttggtcatg caggtttcta caagtgggtc atcaaagact 780  
 tttcaaaagt t 791

<210> 91  
 <211> 264  
 <212> PRT  
 <213> *Gossypium hirsutum*

<400> 91  
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro  
 1 5 10 15  
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys

20										25										30										
Thr	Ser	Ala	Thr	Val	Ile	Glu	Asn	Ser	Ala	Gly	Glu	Ile	Val	Pro	Thr															
35					40					45																				
Arg	Val	Gln	Asn	Gly	Trp	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn															
50					55					60																				
Ser	Leu	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met															
65					70					75					80															
Leu	Glu	Arg	Leu	Ala	Gly	Lys	Ser	His	Tyr	Leu	Glu	Arg	Leu	Ala	Gly															
85					90					95																				
Lys	Ser	His	Tyr	Cys	Cys	Leu	Asp	Gly	Tyr	Glx	Gly	Phe	Phe	Gln	Ile															
100					105					110																				
Pro	Val	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr	Met	Phe	Thr	Cys	Pro	Phe															
115					120					125																				
Gly	Thr	Phe	Ser	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro															
130					135					140																				
Ala	Ser	Phe	His	Arg	Cys	Met	Val	Ser	Ile	Phe	Ser	Asp	Tyr	Val	Asp															
145					150					155					160															
Lys	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Thr	Val	Tyr	Gly	Glu	Ser															
165					170					175																				
Phe	Glu	Val	Ser	Leu	Thr	Asn	Leu	Ala	Lys	Ile	Leu	Glu	Arg	Cys	Leu															
180					185					190																				
Glu	Phe	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Lys	Cys	His	Phe	Met	Val	Asp															
195					200					205																				
Lys	Gly	Leu	Val	Leu	Gly	His	Ile	Ile	Ser	Ala	Asp	Gly	Ile	Ser	Val															
210					215					220																				
Asp	Lys	Ala	Lys	Ile	Asn	Ile	Ile	Asn	Ser	Leu	Pro	Tyr	Pro	Thr	Thr															
225					230					235					240															
Val	Arg	Glu	Ile	Trp	Ser	Phe	Leu	Gly	His	Ala	Gly	Phe	Tyr	Lys	Trp															
245					250					255																				
Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val																							
260																														

<210> 92  
 <211> 763  
 <212> DNA  
 <213> *Gossypium hirsutum*

<400> 92  
 gtgcgtaaag aggtcgtaaa gctacttgat tccgggatga tctatcccat atctgacaat 60  
 aattgggtta gtccagtcca catagtaccc aaaaagaccg gtgtaaccgt aattgagaat 120  
 tcagcaggtg agatggttcc cacttaagtc cgaaacggtc ggagagtatg catcgattac 180

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aggaagttga attccttaac tcggaaagat cactttccac ttctttttat tgatcagatg 240
ttagaacatt tagccagaaa gtctcattat tgttgtctgg atggttactc aggttttttc 300
cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgccc atttggcatg 360
ttcgcttata gaaggatgtc gtttcagact ttgcaatgca ccaaccatgt ttcagaggtg 420
catgataagt atattttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480
tactgtatat agtgagtcct tcgaggtata tttgtcaaat ctagaaaaat ttttggaaag 540
atgcttagaa tttaatcttg ttctaaatta tgagaattgc tatttaattg tagacaaggg 600
attagttcta ggtcatatca tttctgctaa ggggaatttct gtcgataaag taaaaattaa 660
catcataagc tcaataccat accccacaac tgtgaggagg attcgttctt tccttagtca 720
tataggtttc tataggcgat tcatcaagga cttttcaaaa gtt 763

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<210> 93

<211> 254

<212> PRT

<213> *Gossypium hirsutum*

<400> 93

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Val Arg Lys Glu Val Val Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro
  1              5              10              15

Ile Ser Asp Asn Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
      20              25              30

Thr Gly Val Thr Val Ile Glu Asn Ser Ala Gly Glu Met Val Pro Thr
      35              40              45

Glx Val Arg Asn Gly Arg Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60

Ser Leu Thr Arg Lys Asp His Phe Pro Leu Leu Phe Ile Asp Gln Met
      65              70              75              80

Leu Glu His Leu Ala Arg Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr
      85              90              95

Ser Gly Phe Phe Gln Ile Pro Met Ala Leu Lys Asp Gln Glu Lys Met
      100             105             110

Thr Phe Thr Cys Pro Phe Gly Met Phe Ala Tyr Arg Arg Met Ser Phe
      115             120             125

Arg Leu Cys Asn Ala Pro Thr Met Phe Gln Arg Cys Met Ile Ser Ile
      130             135             140

Phe Phe Asp Tyr Val Lys Lys Ile Ile Glu Val Phe Met Asp Glu Phe
      145             150             155             160

Thr Val Tyr Ser Glu Ser Phe Glu Val Tyr Leu Ser Asn Leu Glu Lys
      165             170             175

Phe Leu Glu Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Asn
      180             185             190

Cys Tyr Leu Met Val Asp Lys Gly Leu Val Leu Gly His Ile Ile Ser
      195             200             205

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Ala Lys Gly Ile Ser Val Asp Lys Val Lys Ile Asn Ile Ile Ser Ser  
 210 215 220

Ile Pro Tyr Pro Thr Thr Val Arg Glu Ile Arg Ser Phe Leu Ser His  
 225 230 235 240

Ile Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 94  
 <211> 723  
 <212> DNA  
 <213> Gossypium hirsutum

<400> 94  
 gtgcgtaagg aggttttgaa attggttggat gctggaatga tatactcgat ctttgacagt 60  
 gattgggtta gctgggttca tgctgtgccca aagaaaactg gcgtgacagt ggtgaaaaac 120  
 tcatcaggag agctagtccc taccgagtc cagaatcgat ggagggtttg catcgattac 180  
 aggaagttga acgcagctac ccgaaatgac cattttccac ttcccttcat tgatcaaagt 240  
 ctgcagcgat tagctaataa gacccattat tgttgtctcg atgggtactc aggacttttc 300  
 caaattccgg tggcacctga ggatcaagac aaaacaactt tcacgtgccc ctttggaacg 360  
 tttgcgtata gaagaatgtc gtttggactc tgtaatgctc cggccacttt ccagagatgt 420  
 atggtgagca tattctctga ttatgtcgag aaaatcattg aattcttcat ggatgacttc 480  
 acggtgtacg gtaactcttt taacgaatgt ctgcgataatc ttgctaagat attacagaga 540  
 tgccctagaat ttaactcttg tttaaattat gaaaaatgcc acttcatggg tgacaaagga 600  
 ttaatttttg gtcatatagt ttcttcagaa ggtattgagg tcaataaagc aaaaacgaat 660  
 attattgact cattacctta cccagatgt tacagacgat tcataaagga cttcacaaaa 720  
 gtt 723

<210> 95  
 <211> 241  
 <212> PRT  
 <213> Gossypium hirsutum

<400> 95  
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser  
 1 5 10 15  
 Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys  
 20 25 30  
 Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr  
 35 40 45  
 Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr  
 100 105 110



Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile  
 130 135 140  
 Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe  
 145 150 155 160  
 Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys  
 165 170 175  
 Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys  
 180 185 190  
 Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser  
 195 200 205  
 Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser  
 210 215 220  
 Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys  
 225 230 235 240

Val

<210> 96

<211> 762

<212> DNA

<213> *Lycopersicon esculentum*

<400> 96

gtgcggaaaag aggttgtgaa gctgttagat acgggtattg tctagccaat ttcggacaac 60  
 aagtaggtta gtccagtaca atgtgaacct aaaaagggag acataacggt gatcactaat 120  
 gaaaaaatg agttgatccc aaccatgata gtcacataat ggagaatatg catggattac 180  
 aggaaattga atgaagccac caggaaggac cattaccggg tcccttttat tgatcagatg 240  
 ttggaccggt tggctgggga ataataattat tgttttctta atggctattt acggtacaac 300  
 caaattgtga tttcaccaaa ggattaagag aaaaccactt tcacttgccc gtatgggtaca 360  
 tatgctttca aaaagatacc ttttgggtta tgaaatgcct cggctacttt ccaatgatgc 420  
 atgatggcta tttttcatga tatggttgaa gattttgttg agatattcat gaatgatttc 480  
 tcagtgtttg gggattcttt tgatatgtgc ttggagaatt tggacagtgt gttggctagt 540  
 tgtgaagaaa ctaatctttt cctaaactgg gaataatagc aatttctagt aaaggaaggg 600  
 attatgctag gacataaggt gtcaaagaga ggtatggaag ttgatagtgc caaagtggag 660  
 gttattgaaa agcttcccc tctatatct gttaaaggga tgcaaagttt tctgggtcat 720  
 gttgggttct ataggagatt cataaaagac ttcacaaagg tt 762

<210> 97

<211> 254

<212> PRT

<213> *Lycopersicon esculentum*

<400> 97

Val Arg Lys Glu Val Val Lys Leu Leu Asp Thr Gly Ile Val Glx Pro

1	5	10	15
Ile Ser Asp Asn Lys Glx Val Ser Pro Val Gln Cys Glu Pro Lys Lys	20	25	30
Gly Asp Ile Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr	35	40	45
Met Ile Val Thr Glx Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn	50	55	60
Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met	65	70	75
Leu Asp Arg Leu Ala Gly Glu Glx Tyr Tyr Cys Phe Leu Asn Gly Tyr	85	90	95
Leu Arg Tyr Asn Gln Ile Val Ile Ser Pro Lys Asp Glx Glu Lys Thr	100	105	110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Lys Ile Pro Phe	115	120	125
Gly Leu Glx Asn Ala Ser Ala Thr Phe Gln Glx Cys Met Met Ala Ile	130	135	140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asn Asp Phe	145	150	155
Ser Val Phe Gly Asp Ser Phe Asp Met Cys Leu Glu Asn Leu Asp Ser	165	170	175
Val Leu Ala Ser Cys Glu Glu Thr Asn Leu Phe Leu Asn Trp Glu Glx	180	185	190
Glx Gln Phe Leu Val Lys Glu Gly Ile Met Leu Gly His Lys Val Ser	195	200	205
Lys Arg Gly Met Glu Val Asp Ser Ala Lys Val Glu Val Ile Glu Lys	210	215	220
Leu Pro Pro Pro Ile Ser Val Lys Gly Met Gln Ser Phe Leu Gly His	225	230	235
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val	245	250	

<210> 98

<211> 689

<212> DNA

<213> Lycopersicon esculentum

<400> 98

cgaaaggagg tgggtgaaact ggaaattatc aagtagttgg atgctagagt aatctatcca 60  
atcgccgata gtagttgggt atgcctagtt cagtgtgtac caaagaaagg gggaatgact 120  
gtggtcccca acgaaaagaa tgaacttggt cgaatgagac cggttactgg atggaggggtg 180

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tgc atg gatt acc gtaa act ga act ca tag act gaaaaa g act at tttt ca tat gcc cttc 240
at gg at caga tg tt gg at ag act t gcc gg aa ag gg tg gt att g tttt ct tg at gg gt at 300
tc ggg gt ata at ca ga tttc tat tgc acca ga ag at ca ag ag aaaa acc ac ttt cact tgt 360
cc ata cg gg a ctt tt tgc att ca ga aga at g tc gtt tgg gt tgt gca at gc acc cg ca acc 420
ttt ca ga gat gg at ga tgc aat at tttt ct ga cat ga tgg ag ga ta ct at ag ag gtt ttt 480
at gg at gatt ttt ct gt gg t gg t ga ttc a ttc ga gc gg t gct tgc tcaa ttt at ct ga g 540
gtt ct ta aga gat gt ga aga ct gca att t g ta ct aa act ggg aaa ag tgc att ttc at g 600
gt gaa ag ag g gt att gt gt g gg t ca tgc at ttc a gaaa ag gg ca tgc a tg tttt t act 660
gg t ga ttc at caa ag act t c acaa ag gt t 689

```

<210> 99

<211> 229

<212> PRT

<213> *Lycopersicon esculentum*

<400> 99

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Arg Lys Glu Val Val Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala Arg
  1                      5                      10                      15

```

```

Val Ile Tyr Pro Ile Ala Asp Ser Ser Trp Val Cys Leu Val Gln Cys
          20                      25                      30

```

```

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Glu Lys Asn Glu
          35                      40                      45

```

```

Leu Val Arg Met Arg Pro Val Thr Gly Trp Arg Val Cys Met Asp Tyr
          50                      55                      60

```

```

Arg Lys Leu Asn Ser Glx Thr Glu Lys Asp Tyr Phe His Met Pro Phe
          65                      70                      75                      80

```

```

Met Asp Gln Met Leu Asp Arg Leu Ala Gly Lys Gly Trp Tyr Cys Phe
          85                      90                      95

```

```

Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ser Ile Ala Pro Glu Asp
          100                     105                     110

```

```

Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Arg
          115                     120                     125

```

```

Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Trp
          130                     135                     140

```

```

Met Met Ser Ile Phe Ser Asp Met Met Glu Asp Thr Ile Glu Val Phe
          145                     150                     155                     160

```

```

Met Asp Asp Phe Ser Val Val Gly Asp Ser Phe Glu Arg Cys Leu Ser
          165                     170                     175

```

```

Asn Leu Ser Glu Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
          180                     185                     190

```

```

Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Val Leu Gly
          195                     200                     205

```

```

His Arg Ile Ser Glu Lys Gly Met His Val Phe Thr Gly Asp Ser Ser

```

210

215

220

Lys Thr Ser Gln Arg  
225

&lt;210&gt; 100

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Lycopersicon esculentum

&lt;400&gt; 100

```

gtgcgtaagg aggtgtttaa gcttctagat gcgggtattg tctacccaat taggacaaca 60
agtgggttag tctagtacaa tgtgtaccta aaaagggagg catggcaatg attactaatg 120
aaaacaatga gtttatccca accagcacag tcacaagatg gcgaatatgc atgaattaca 180
cgaagttaat gaagccacta ggaagaatca ttacccaatt ctttttattg attatatgtt 240
ggaccggtta gctgggcaag aatattattg ttttttggat tactaatcag ggtacaacta 300
aattttgatt gcaccagagg atcaagagaa aacaactttc acttgcccgt atggtagata 360
tgctttcaag aggatacctt ttgggttatg caatgctctg tctaatttcc aaagatgcat 420
gatgactatt tttcatgata tggttgaata ttttgaggat atattcatgg atgatttctt 480
agtgttttgg gagtcttttg atagatgctt ggagaatttg aacaggttgt tagctagggtg 540
cgaacaaact aatcttgtcc tgaactggga aaaatgtcat tttttagtaa aggaagggaa 600
tttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtggaagt 660
aattgaaaag atctcctctc ccatttttgt gaaacgggtg agaagtttac taggtcatgc 720
tgagttttac aggatattca tcaaggactt ctcaaagggtt 760

```

&lt;210&gt; 101

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Lycopersicon esculentum

&lt;400&gt; 101

```

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
  1             5             10             15

Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys
      20             25             30

Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr
      35             40             45

Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn
      50             55             60

Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met
      65             70             75             80

Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx
      85             90             95

Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr
      100            105            110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe
      115            120            125

```

Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile  
 130 135 140  
 Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe  
 145 150 155 160  
 Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg  
 165 170 175  
 Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx  
 195 200 205  
 Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys  
 210 215 220  
 Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His  
 225 230 235 240  
 Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 102  
 <211> 776  
 <212> DNA  
 <213> *Lycopersicon esculentum*

<400> 102  
 gtgcggaaag aagtgtttta actggaatca ttaaattggtt ggatgctgga gtaatatatc 60  
 cgatctccga tagtagttgg gtatgcccta ttcagtgtgt acctaagaaa gggggaatga 120  
 ctgtgggtccc caataagaaa aatgaacttg ttctaattgag accggttact ggaggggtggg 180  
 tgtgtattgga ttaccgtaaa ttaaattgcat ggactgaaaa agaccatttt cctatgccct 240  
 tcatggatca gatgttggat agacttgccg aaaaagggtg gtactgtttt cttgatggat 300  
 agtcagggtg taattagatt tctattgcac cagaagatca agagaaaacc acatttactt 360  
 gtccatatgg gaccttttga ttgaagagaa tgtcgttttg gttgtgcaat gcacccgcca 420  
 catttcacag atgtaaaaat gttgatattc ttcgacatgg tggatgatac tattgatgct 480  
 tttatggatg atttttctct tgttggtgaa tcattcgaga ggtgtttgaa ccatttatct 540  
 gatgtcctta agagatgtga agactgcaat ttagtactaa attgggaaaa atgccacttc 600  
 atggtgaaaa aaggtattgt tttgggtcat cgcattccag aaaagggtcat agaggttgat 660  
 cgagctaaaag tagaggtaat agagagactt cccccactat ctctgtaaaa ggtgtgagaa 720  
 gctttcttgg gcatgcaagt ttttaccgga gattcatcaa agacttcaca aaagtt 776

<210> 103  
 <211> 258  
 <212> PRT  
 <213> *Lycopersicon esculentum*

<400> 103  
 Ala Glu Arg Ser Val Glx Thr Gly Ile Ile Lys Trp Leu Asp Ala Gly  
 1 5 10 15  
 Val Ile Tyr Pro Ile Ser Asp Ser Ser Trp Val Cys Pro Ile Gln Cys  
 20 25 30

Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Lys Lys Asn Glu  
 35 40 45  
 Leu Val Leu Met Arg Pro Val Thr Gly Gly Trp Val Cys Met Asp Tyr  
 50 55 60  
 Arg Lys Leu Asn Ala Trp Thr Glu Lys Asp His Phe Pro Met Pro Phe  
 65 70 75 80  
 Met Asp Gln Met Leu Asp Arg Leu Ala Glu Lys Gly Trp Tyr Cys Phe  
 85 90 95  
 Leu Asp Gly Glx Ser Gly Tyr Asn Glx Ile Ser Ile Ala Pro Glu Asp  
 100 105 110  
 Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Leu Lys  
 115 120 125  
 Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe His Arg Cys  
 130 135 140  
 Lys Met Leu Ile Phe Phe Asp Met Val Asp Asp Thr Ile Asp Ala Phe  
 145 150 155 160  
 Met Asp Asp Phe Ser Leu Val Gly Glu Ser Phe Glu Arg Cys Leu Asn  
 165 170 175  
 His Leu Ser Asp Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu  
 180 185 190  
 Asn Trp Glu Lys Cys His Phe Met Val Lys Lys Gly Ile Val Leu Gly  
 195 200 205  
 His Arg Ile Pro Glu Lys Gly Ile Glu Val Asp Arg Ala Lys Val Glu  
 210 215 220  
 Val Ile Glu Arg Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser  
 225 230 235 240  
 Phe Leu Gly His Ala Ser Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr  
 245 250 255

Lys Val

<210> 104  
 <211> 761  
 <212> DNA  
 <213> Solanum tuberosum

<400> 104  
 gtgcggaagg aggtacttaa attgttggat gcacggattg tgtacccaat atcagacagt 60  
 aaatgggttaa gtccagtaaa gtgtgtgccc aagaaggcca gaatgacggt gttgactaat 120  
 gagaagaatg aggtaatccc cacaagaaca gtgactgggt gacggatttg catggactac 180  
 atgaagttga acgacgccac cagaaaggac cattatccgg tacctttcat tgataaaata 240

ttggataggt tggcaggaca tgagtactat tgttttcttg gtgtctactc aggggtacaat 300  
 cagattgtta ttgcaataga ggactaggtg aaaaccacct tcacctgttc gtatggcaca 360  
 tatgCGttca agcacatgcc attcggtcttg tgcaatgccc tggccacatt tcagagatgc 420  
 atgttggcaa tcttccatga tatggtggag gattttgttg aagttttcat ggatgacttc 480  
 ttggtgtttg gtgagtcttt tgaactttgt ttgactaatt ttgacagatt tcttgctagg 540  
 tgtgaagaga cgaatctggt gataaactga tagaagtgtc actttctggt tcgagagggga 600  
 attgtgttg gacacaagat ctccaaaaat gggctgaaag ttgacaaagc caacgtagag 660  
 gttattgaga aattgccacc cccatcacag tgaaggtaat taaaagctta ctaggacatg 720  
 cttggtttta tacgagggtc atcaaagact tcacaaaggt t 761

<210> 105  
 <211> 254  
 <212> PRT  
 <213> Solanum tuberosum

<400> 105

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Arg Ile Val Tyr Pro  
 1 5 10 15

Ile Ser Asp Ser Lys Trp Val Ser Pro Val Lys Cys Val Pro Lys Lys  
 20 25 30

Gly Arg Met Thr Val Leu Thr Asn Glu Lys Asn Glu Val Ile Pro Thr  
 35 40 45

Arg Thr Val Thr Gly Glx Arg Ile Cys Met Asp Tyr Met Lys Leu Asn  
 50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Lys Ile  
 65 70 75 80

Leu Asp Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Gly Val Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Ile Ala Ile Glu Asp Glx Val Lys Thr  
 100 105 110

Thr Phe Thr Cys Ser Tyr Gly Thr Tyr Ala Phe Lys His Met Pro Phe  
 115 120 125

Gly Leu Cys Asn Ala Leu Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
 130 135 140

Phe His Asp Met Val Glu Asp Phe Val Glu Val Phe Met Asp Asp Phe  
 145 150 155 160

Leu Val Phe Gly Glu Ser Phe Glu Leu Cys Leu Thr Asn Phe Asp Arg  
 165 170 175

Phe Leu Ala Arg Cys Glu Glu Thr Asn Leu Val Ile Asn Glx Glx Lys  
 180 185 190

Cys His Phe Leu Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205

Lys Asn Gly Leu Lys Val Asp Lys Ala Asn Val Glu Val Ile Glu Lys

210

215

220

Leu Pro Pro Pro Ile Thr Val Lys Val Ile Lys Ser Leu Leu Gly His  
 225 230 235 240

Ala Trp Phe Tyr Thr Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

&lt;210&gt; 106

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 106

gtgcgtaaag aggtttttcaa actgctagat gtcggtattg tatatccgat ttcagaaaagc 60  
 aaatgggtca gccagtttta gtgtgtgcct aaaaaaagag gcatgccggt gatcaccaat 120  
 gaaaaaaatg agttgattcc aaccaggaca gtgacagggt ggcgaatatg catggattat 180  
 aggaaattga atgaggccac cagaaaggat cactgcccgg ttccttttat tgatcagatg 240  
 ctggacaggt tagttgggca agaataattat tgtttcctgg aaggctattc aggatacaac 300  
 caaattgtga ttgcaccaga ggaccaggag aaaactacat tcacttgtct gtatgggaca 360  
 tatgctttca agtgactgcc gtttgggcta tgcaatgctc cagccacctt ccaaagatga 420  
 atgatggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480  
 tcagtcttta gggagtcttt tgataggtgt ttggagaatt gggacagggt gctggctaga 540  
 tgcgaggaaa ctaatctcat cctaaactgg aaaaaatgtc atttcctagt aaatgaaggg 600  
 attgtattgg gccataaggt gtcaaagaga gggctggaag ttgatcgtgc caaagtggaa 660  
 gttattgaaa aactacctcc tccaatctgt taaaggggtg agaagctttc tgggtcatgc 720  
 tggtttttac aggagattta taaaggactt cacaaaaggtt 760

&lt;210&gt; 107

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 107

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Val Tyr Pro  
 1 5 10 15

Ile Ser Glu Ser Lys Trp Val Ser Pro Val Glx Cys Val Pro Lys Lys  
 20 25 30

Arg Gly Met Pro Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
 35 40 45

Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn  
 50 55 60

Glu Ala Thr Arg Lys Asp His Cys Pro Val Pro Phe Ile Asp Gln Met  
 65 70 75 80

Leu Asp Arg Leu Val Gly Gln Glu Tyr Tyr Cys Phe Leu Glu Gly Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Glu Lys Thr  
 100 105 110



Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Ala Phe Lys Glx Leu Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Glx Met Met Ala Ile  
 130 135 140  
 Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Phe Arg Glu Ser Phe Asp Arg Cys Leu Glu Asn Trp Asp Arg  
 165 170 175  
 Val Leu Ala Arg Cys Glu Glu Thr Asn Leu Ile Leu Asn Trp Lys Lys  
 180 185 190  
 Cys His Phe Leu Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 108  
 <211> 761  
 <212> DNA  
 <213> Solanum tuberosum

<400> 108  
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 aaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180  
 gaaaattaaa tgaagctacc agaaaggatc actaccgggt tccttttatt gatcagatgc 240  
 tggacagggt ggctggacaa gaatattatt gtttcttggg tggttattca ggatacaacc 300  
 aaatagtgat tgcaccagag gaccagggga aaactacatt cacttgcttg tatgggacat 360  
 atgtttccaa gagaatgtcg tttgggctat gcaatgctcc atccattttc caaagatgca 420  
 tgatggccat cttccatgat aagggttgaag attttatgga aatattcatg gatgacttct 480  
 cagtatttgg ggagtctttt gacagggtgct tggagaattt agacagagtg ttggctagat 540  
 gcgaggaaac taattttgtc ctaaactggg aaaaatgtca tttcctagtg aaggaaggga 600  
 ttgtgttggg tcataagggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660  
 taatcaaaaa gctacctccc ccaatttctg ttaaaggggt gcgaagtttt ttgggtcatg 720  
 ttagtttcta cgaaagattc ataaaggact tcaccaagggt t 761

<210> 109  
 <211> 254  
 <212> PRT  
 <213> Solanum tuberosum

<400> 109  
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro  
 1 5 10 15

Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys  
                     20                    25                    30  
 Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
                     35                    40                    45  
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn  
                     50                    55                    60  
 Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met  
                     65                    70                    75                    80  
 Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
                     85                    90                    95  
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr  
                     100                    105                    110  
 Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe  
                     115                    120                    125  
 Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile  
                     130                    135                    140  
 Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe  
                     145                    150                    155                    160  
 Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg  
                     165                    170                    175  
 Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys  
                     180                    185                    190  
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser  
                     195                    200                    205  
 Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys  
                     210                    215                    220  
 Leu Pro Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
                     225                    230                    235                    240  
 Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val  
                     245                    250

<210> 110

<211> 762

<212> DNA

<213> Solanum tuberosum

<400> 110

gtgcgtaagg aggtcctcaa gctgtctgat gcaggaattg tgtaccccat ttatgatata 60  
 aagtggatca gccagttca ctgtgtgccg aaaaaggag gcatgacgat tattactaat 120  
 gaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180  
 aggagactaa atgaggcaac tagaaaggaa cactaccag ttcctttcat tgatcaaatg 240

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ttggacaggt ttattgggca agagtattat tgtttcctag atggctattc aggatataat 300
caaattgtga ttgcgccata agataaagag aaaactacat ttacttctct atatgggaca 360
tatgccttca agagaatgtc gtttgggccg tgcaatgctc caaccacatt ccaaagatgc 420
atgacagcca tttttcatga tatgggtcaaa tattttgtgg agatattcat ggatgaattc 480
ttagtctttg gggagtcttt tgacacgtgt ctagaatatt tggacaatgt gcttgccaga 540
tgtgaggaaa ctaatcccg cctcaactgg gaaaaatgtc attttctagt gaagaagggg 600
attgtactag gccacaaggt ttcagaggaa ggactggaag ttgatcgtgg aaaagtagag 660
gtaatttaaa agctaccccc tcaagtcttc gttaaagggg tgagaagggt ccttggtcat 720
tctaggttcg aaatgagatt cataaaagac ttcacaaaag tt 762

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<210> 111  
 <211> 254  
 <212> PRT  
 <213> Solanum tuberosum

<400> 111  
 Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro  
 1 5 10 15  
 Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala  
 35 40 45  
 Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn  
 50 55 60  
 Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe  
 115 120 125  
 Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile  
 130 135 140  
 Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe  
 145 150 155 160  
 Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn  
 165 170 175  
 Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys

210	215	220
Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His		
225	230	235 240

Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 112  
 <211> 762  
 <212> DNA  
 <213> Solanum tuberosum

<400> 112  
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 gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggcgaaatag catggattat 180  
 atgaagtga atgaggccac cagaaaggat cactaccga ttcattttat tgatcagatg 240  
 ttggacaagt tagctgagta aaaatattat tgtttcttgg cttgttattc aagatacaac 300  
 caatttctca ttgcaccaca ggaccaggag gaaactacat tcaactgtcc ttatgggaca 360  
 tatgctttca agcgaatgtc gtttgggcta tgcaatgctc caaccacctt ccaaagatgc 420  
 ataagggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480  
 tcagtctttg ggtagtcttt tgagaggtgt ctggaaaatt ttgacagggt gctggctgta 540  
 tgcgaggaaa ctaatttttt cctaaactgg gaaaaatgct attttctagt gaaggaaggg 600  
 attgtattgg gacataaggt gtcaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660  
 gtcgttgaaa acctaccttc cccattctct gttaaagggg tgagaagttt tttgggtcat 720  
 gctggtttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113  
 <211> 254  
 <212> PRT  
 <213> Solanum tuberosum

<400> 113  
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln  
 1 5 10 15  
 Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys  
 20 25 30  
 Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr  
 35 40 45  
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn  
 50 55 60  
 Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr  
 85 90 95  
 Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Thr  
 100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Ile Arg Ala Ile  
 130 135 140  
 Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg  
 165 170 175  
 Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn  
 210 215 220  
 Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 114  
 <211> 793  
 <212> DNA  
 <213> Solanum tuberosum

<400> 114  
 aacttttgtg aagtcttttaa tgaaggatgt tgtcagagaa gaagtcatca agtggctgga 60  
 tacagggatt gtgtacccaa tatctgacaa taaatgggca agtccagtgc agtgtgtgcc 120  
 taaaaagggg ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac 180  
 agtaactggg tggaggctat gcatggacta cagaaaactc aatgaagcca ccaggaagga 240  
 ccactattcg gtaccgttca ttgatcaaat gttagacagg ttggctggcc aagagtatta 300  
 ctgtttcctt gatggttatt caagggtataa ttagatcgtc attgcacctg aggatcaaga 360  
 gaatacgaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggtctt 420  
 gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgga 480  
 agattttgtt aaagtataca tggacgattt ctcggtgttt ggtgagtcgt tcgaactttg 540  
 tttatctaata cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg 600  
 ggagaagtgt cactttcttg tcagagaagg aattatgttg gggcagaaga tctccaaaag 660  
 tgggctagaa gtagacaagg cgaagggtgga agtgattgag aagttgccac caccaatata 720  
 agtaaaggga gtgcgaagct tccttggaca tgctgggttt tacaagaggt tcataaagga 780  
 cttttcaaag gtt 793

<210> 115  
 <211> 264  
 <212> PRT  
 <213> Solanum tuberosum

<400> 115  
 Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile

1	5	10	15
Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp	20	25	30
Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val	35	40	45
Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp	50	55	60
Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp	65	70	75
His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly	85	90	95
Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile	100	105	110
Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr	115	120	125
Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro	130	135	140
Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu	145	150	155
Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser	165	170	175
Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu	180	185	190
Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg	195	200	205
Glu Gly Ile Met Leu Gly Gln Lys Ile Ser Lys Ser Gly Leu Glu Val	210	215	220
Asp Lys Ala Lys Val Glu Val Ile Glu Lys Leu Pro Pro Pro Ile Glx	225	230	235
Val Lys Gly Val Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Arg	245	250	255
Phe Ile Lys Asp Phe Ser Lys Val	260		

<210> 116

<211> 761

<212> DNA

<213> Platanus occidentalis

<400> 116

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gtgcgtaagg aggttttcaa acttcttaaa gtttgagtga tttatcctat ttaggatagg 60
aattgggtca gcccggttca agtgggtcct aaaaagattg gaataaccgt tgtgaaaaat 120
tagaatgatg agttgggtcc taccagtgtt cagaatgggt ggaggggtgt atagattata 180
gaaaattgaa tgttgtaacc cgcaaggatc acttcccttt accttttatt gatcaaatgc 240
ttgaaagggt agttgggtcat tcttactatt gtttcctaga tggttattca agttatttcc 300
agattgtaat tactccagag gattaagaaa agacaacttt tacatgtcca tttgggactt 360
ttgcatatcg ttgcatgccc tttggccttt gcaatgcccc aaccactttc caaagggtga 420
tggtttagcat attttcatat tacattgaga atatcataga agtttttatg gatgatttca 480
tagtttatgg agactccttt aataattttc tgcataacct tacacttggt cttcaaagat 540
gcatagaaac taaccttggtg ttaaattatg aaaaatgtca ttttatgggt gaacaaggta 600
tagttttggg tcatggttatt tcactctaaag gaattgaggt agataaagct aaagttgata 660
ttattcaatc tttaccttat ctcattagta tgcggaaagt tcattctttt cttggacatg 720
caggtttcta ccgaagattc attaaagact ttacaaagggt t 761

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<210> 117

<211> 254

<212> PRT

<213> *Platanus occidentalis*

<400> 117

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Val Arg Lys Glu Val Phe Lys Leu Leu Lys Val Glx Val Ile Tyr Pro
  1              5              10              15

Ile Glx Asp Arg Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20              25              30

Ile Gly Ile Thr Val Val Lys Asn Glx Asn Asp Glu Leu Val Pro Thr
      35              40              45

Ser Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60

Val Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
      65              70              75              80

Leu Glu Arg Leu Val Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85              90              95

Ser Ser Tyr Phe Gln Ile Val Ile Thr Pro Glu Asp Glx Glu Lys Thr
      100             105             110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Cys Met Pro Phe
      115             120             125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Val Ser Ile
      130             135             140

Phe Ser Tyr Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe
      145             150             155             160

Ile Val Tyr Gly Asp Ser Phe Asn Asn Phe Leu His Asn Leu Thr Leu
      165             170             175

Val Leu Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Tyr Glu Lys
      180             185             190

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Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Ile Ser  
 195 200 205

Ser Lys Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ile Ile Gln Ser  
 210 215 220

Leu Pro Tyr Leu Ile Ser Met Arg Lys Val His Ser Phe Leu Gly His  
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 118  
 <211> 762  
 <212> DNA  
 <213> Platanus occidentalis

<400> 118  
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 aattgggtta gcccagttca agtggctcct aaaaagactg gaataaccgt tgtgaaaaat 120  
 cagaatgatg agttagttcc tacccatggt cagaatgggt ggtgggtttg tataaattat 180  
 agaaaattaa atgttataac ctgcaaggat cacttccctt taccttttat tgataaaatg 240  
 cttgaaaggt tagctgggtca ttcttactat tgtttccttg atggttatatt aggttatattt 300  
 caaattgcaa ttacttcgga ggatcaagaa aagatgattt ttaagtgcc attcgggact 360  
 tttgcataac gtcacatgcc ctttggcctt tgcaatgccc caaccacttt ctaaagggtgt 420  
 atggtttagca tattttcaga ttacattgag aatatcatag aagtctttat ggatgatttc 480  
 acagtttatg gagactcctt tgataattgt ctgcataacc ttacacttgt tattcaaaga 540  
 tgcatagaaa ctaacctagt gttaaattct taaaaatgtc attttatggt tgaacaagggt 600  
 atagtttttg gtcattgtgt ttcatctagg ggaattgagg tagataaacc taaagttgat 660  
 attattcaaa ctttacctta ttccactagt gtgcgagaag ttctgtcttt tcttggacat 720  
 gtaggttttt actgaagatt cataaaaagac ttcacaaagg tt 762

<210> 119  
 <211> 254  
 <212> PRT  
 <213> Platanus occidentalis

<400> 119  
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Val Gly Val Ile Tyr Leu  
 1 5 10 15  
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val Gln Val Ala Pro Lys Lys  
 20 25 30  
 Thr Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr  
 35 40 45  
 His Val Gln Asn Gly Trp Trp Val Cys Ile Asn Tyr Arg Lys Leu Asn  
 50 55 60  
 Val Ile Thr Cys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Lys Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95



Leu Gly Tyr Phe Gln Ile Ala Ile Thr Ser Glu Asp Gln Glu Lys Met  
 100 105 110  
 Ile Phe Lys Cys Pro Phe Gly Thr Phe Ala Tyr Arg His Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Cys Met Val Ser Ile  
 130 135 140  
 Phe Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Thr Val Tyr Gly Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu  
 165 170 175  
 Val Ile Gln Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Ser Glx Lys  
 180 185 190  
 Cys His Phe Met Val Glu Gln Gly Ile Val Leu Gly His Val Val Ser  
 195 200 205  
 Ser Arg Gly Ile Glu Val Asp Lys Pro Lys Val Asp Ile Ile Gln Thr  
 210 215 220  
 Leu Pro Tyr Ser Thr Ser Val Arg Glu Val Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Val Gly Phe Tyr Glx Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 120  
 <211> 759  
 <212> DNA  
 <213> *Platanus occidentalis*

<400> 120  
 gtgcggaaaag aggttttttaa gcttttggat gtagggatta tatacccaat tttttatagt 60  
 aattaggtaa gtcccaactca agtggaccca agaattctgg tgtgactgta gttaaaaatg 120  
 caaatgatga attgattcca aatagactca ctattgggttg gcgtgtatgc attaactata 180  
 agaagttgaa ctcaagtact aggaaggacc atttcccttt accattcatg actaaatcct 240  
 agaaagggtta gctggtcaca aattttatta tttcctatat ggttattcta gatataacta 300  
 aatagagatt gcacctgagg actaagaaaa taccactttt acatgtccat ttggcacttt 360  
 tgcttatcga aggatgtcat ttggattatg taatgctctt gccacgttct aaagatgcat 420  
 gttgagtata tttagtata tggtagaaca ttttcttgag gtgtttatgg attttttttg 480  
 tttttggttaa ttcatttgat gattgtttgc ataatttgaa aaaagtgtta aatagatgtg 540  
 aaggaaaaaaa acatcatttt gaattgagag aagtgtcatt tcatggcttc taaaagaatt 600  
 gtacttggtc acattgtctc ctcccaagga attaaagtgg tcaaagccaa aattgaattg 660  
 atagtcaatt tgccatgccc aaagactcct aaagacattc gatcttttct aggtcatgca 720  
 ggatttaaca aaaggttcat caaagacttc acgaaagtt 759

<210> 121  
 <211> 254  
 <212> PRT  
 <213> *Platanus occidentalis*

<400> 121

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro  
1 5 10 15

Ile Phe Tyr Ser Asn Glx Val Ser Pro Thr Gln Val Val Pro Lys Asn  
20 25 30

Ser Gly Val Thr Val Val Lys Asn Ala Asn Asp Glu Leu Ile Pro Asn  
35 40 45

Arg Leu Thr Ile Gly Trp Arg Val Cys Ile Asn Tyr Lys Lys Leu Asn  
50 55 60

Ser Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Glx Ile  
65 70 75 80

Leu Glu Arg Val Ala Gly His Lys Phe Tyr Tyr Phe Leu Tyr Gly Tyr  
85 90 95

Ser Arg Tyr Asn Glx Ile Glu Ile Ala Pro Glu Asp Glx Glu Asn Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ala Thr Phe Glx Arg Cys Met Leu Ser Ile  
130 135 140

Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys  
165 170 175

Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys  
180 185 190

Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser  
195 200 205

Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn  
210 215 220

Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 122

<211> 761

<212> DNA

<213> Platanus occidentalis

<400> 122

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tcgcgtaaaga ggtgggtcaag cttcttgaag ttggagtgat ttatcctatt tcggatagca 60
attggggttag cccgggttcaa gtgggttccta aaaagactgg aataaccgtt gtgaaaaatc 120
aaaatgatga gttagttcct acccgtgttc agaatgggtg gcaggtttgt atagattata 180
taaaattaaa tggtgtaacc cgcaaggatc acttcccttt accttttatt gatcaaatgt 240
ttgaaagggtt agctgggtcat tcttactatt gtttccttga tggatattca tgttattttt 300
agattgcaat tactccagag gatcaagaaa agacgacttt tacgtgcccc ttcggggactt 360
tttcatatcg ttgcatgccc tttggccttt gcaacgcccc agccactttc caaagggtga 420
tggtttagcat attttcagat tacattgaga atatcataga agtctttatg gatgatttca 480
tagtttatga agactccttt gataattgtc tgcataacct tacacttggt ttttaaagat 540
gcatagaaac taaccttgtg ttaaattttg aaaaatgtca tggtatgggt gaataaggta 600
tagttttggg tcatgttgtt tcatctatgg gaattgaggt agataaagtt aaagttgata 660
ttattcaatc tttaccttat cccattagtg tgcaggaaagt tcgttctttt cttggacatg 720
cgggttttta ccaaagattc attaaagact tcacgaaagt t 761

```

<210> 123  
 <211> 253  
 <212> PRT  
 <213> *Platanus occidentalis*

<400> 123  
 Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Val Ile Tyr Pro Ile  
 1 5 10 15  
 Ser Asp Ser Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Thr  
 20 25 30  
 Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr Arg  
 35 40 45  
 Val Gln Asn Gly Trp Gln Val Cys Ile Asp Tyr Ile Lys Leu Asn Val  
 50 55 60  
 Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met Phe  
 65 70 75 80  
 Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser  
 85 90 95  
 Cys Tyr Phe Glx Ile Ala Ile Thr Pro Glu Asp Gln Glu Lys Thr Thr  
 100 105 110  
 Phe Thr Cys Pro Phe Gly Thr Phe Ser Tyr Arg Cys Met Pro Phe Gly  
 115 120 125  
 Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile Phe  
 130 135 140  
 Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe Ile  
 145 150 155 160  
 Val Tyr Glu Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu Val  
 165 170 175  
 Phe Glx Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Phe Glu Lys Cys  
 180 185 190

His Val Met Val Glu Glx Gly Ile Val Leu Gly His Val Val Ser Ser  
 195 200 205

Met Gly Ile Glu Val Asp Lys Val Lys Val Asp Ile Ile Gln Ser Leu  
 210 215 220

Pro Tyr Pro Ile Ser Val Gln Glu Val Arg Ser Phe Leu Gly His Ala  
 225 230 235 240

Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 124  
 <211> 761  
 <212> DNA  
 <213> Sorghum bicolor

<400> 124  
 gtgcgtaaag aggtcttcaa gctctatcat gctgggatta tttatcctgt gccgcatagt 60  
 gagtgggtta gccctgttca agtagtgcca aagaaaggag gaatgacggt cgtaggaat 120  
 gagaagaatg aactcatccc tcaacgaatt gtcactgggt ggcgtatgtg tattgactat 180  
 caaaaactca acacggctac aaagaaagat aactttccgt tacccttcat tgatgaaatg 240  
 ttggaacggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300  
 caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtatggaact 360  
 tatgcataac gacgaatgtc gttcggactg tgcaatgctc cagcttcttt ccaacgggtgc 420  
 atgatgtcta ttttctcgga catgattgag aagatcatgg aggttttcat ggatgatttt 480  
 accgtctatg gtaaaacctt cgatcattgt ttggagaatt tagatagagt cttgcagcga 540  
 tgtgaagaaa agcacttaac cctgaactgg gagaaatgcc attttatggt tcaggaagga 600  
 atagtgctag gacataaagt gtccgaacgt ggtatagagg tggacaaagc aaagattgaa 660  
 gttattgaaa aacttccacc tcccacgaat gtgaaaggat ccgtagcttc ttgggacatg 720  
 caggggttcta tagatgcttc ataaaagact tcacaaagggt t 761

<210> 125  
 <211> 254  
 <212> PRT  
 <213> Sorghum bicolor

<400> 125  
 Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro  
 1 5 10 15  
 Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn  
 50 55 60  
 Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr  
 100 105 110  
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Glx Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
 130 135 140  
 Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Thr Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Cys Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 126  
 <211> 762  
 <212> DNA  
 <213> Sorghum bicolor

<400> 126  
 gtgcggaagg aggtccttaa attgctgcat gcagggatta tatatcctgt gccgcacagt 60  
 gagtgggtga gcccagtaca agttgtgcct aaaaaaggag gcatgactgt tattataaat 120  
 gaaaagaacg agctaattcc gcaacgcacc gtcacaggat ggcagatgtg catagactat 180  
 agaaaactaa acaaaagccac gagaaaaggat cacttttcctt taccttttat agatgagatg 240  
 ctagagcggg tagcaaacca ttcgttcttc tgtttcttag atggatatcc agggatatcat 300  
 cagatcccga tccatcccga tgatcaaagc aaaaccactt ttacatgccc ttatggaact 360  
 tatgcttacc gtagaatgtc ttttgggtta tgtaatgcac cagcttcttt tcaaagatgc 420  
 atgatgtcta tattttctga tatgattgaa gagattatgg aagttttcat ggatgatttc 480  
 tctgtttatg gaaaagcttt tgatagttgt cttgaaaact tagacaagg tttgcaaagt 540  
 tgtgaagaaa agcacttaac ccttaattgg gaaaaatgtc attttatggt tagggaagga 600  
 atagtgttag gacacttagt gtctgaaagg ggtattgagg tagacaaagc tgaaattgaa 660  
 gtaattgaac aactacctcc acctgtgaat ataaaaggaa ttcgaagctt tcttggccat 720  
 gctgggtttt atcgtagatt catcaaagat ttcacgaaag tt 762

<210> 127  
 <211> 254  
 <212> PRT  
 <213> Sorghum bicolor

<400> 127

Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Ile Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Arg Thr Val Thr Gly Trp Gln Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Glu Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Tyr Gly Lys Ala Phe Asp Ser Cys Leu Glu Asn Leu Asp Lys  
165 170 175

Val Leu Gln Ser Cys Glu Glu Lys His Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser  
195 200 205

Glu Arg Gly Ile Glu Val Asp Lys Ala Glu Ile Glu Val Ile Glu Gln  
210 215 220

Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 128

<211> 762

<212> DNA

<213> Sorghum bicolor

<400> 128

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gtgcggaagg aagtcttaaa gcttttacac actaggatta tttatctcgt tcctcatagt 60
gagtgggtta gcacggtaca agttgtgcca aagaaaggag gaatgtcggg tgtaggaat 120
gagaagaacg aattcatccc tcaacaaact gtcactgggt ggcgtatgtg cattgactac 180
caaaaactca acaaggccac aaggaaagat cacttcccgt tacctttcat tgatgaaatg 240
ttgtaatggc ttacaaatca ctcgttcttt tgtttccttg aagggtattc cagatatcat 300
caaatcccgga tccaccacga tgaccaaagt aagactactt tcacatgacc ctatggaact 360
tacgcatacc gacgaatgtc gttcagggtta tgtaatgctc cagcttcttt tcaacgggtgc 420
atgatgtcta ttttttccaa tatgattgag aaaatcatgg aggtattcac ggatgatttt 480
accgtatatg gcaaaacctt tgatgattgt ttagagaatt tggacaaagt cttacaattg 540
tgtgaaggaa agcacttaat cgtaaactag gagaaatgcc attttatggt ccgagaagga 600
atagtgctag ggcacaaggt gtccgaacgt gggatagagg tggatagagc caagattgaa 660
gttattgaaa aacttccacc tcccacaaat gtgaaagaca tccgcagttt tcttggacat 720
gcagggttct ataggcgctt catcaaagat ttcaccaagg tt 762

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<210> 129  
 <211> 254  
 <212> PRT  
 <213> Sorghum bicolor

```

<400> 129
Val Arg Lys Glu Val Leu Lys Leu Leu His Thr Arg Ile Ile Tyr Leu
  1                      5                      10                      15

Val Pro His Ser Glu Trp Val Ser Thr Val Gln Val Val Pro Lys Lys
          20                      25                      30

Gly Gly Met Ser Val Val Arg Asn Glu Lys Asn Glu Phe Ile Pro Gln
          35                      40                      45

Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
  50                      55                      60

Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
  65                      70                      75                      80

Leu Glx Trp Leu Thr Asn His Ser Phe Phe Cys Phe Leu Glu Gly Tyr
          85                      90                      95

Ser Arg Tyr His Gln Ile Pro Ile His His Asp Asp Gln Ser Lys Thr
          100                      105                      110

Thr Phe Thr Glx Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe
          115                      120                      125

Arg Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
          130                      135                      140

Phe Ser Asn Met Ile Glu Lys Ile Met Glu Val Phe Thr Asp Asp Phe
          145                      150                      155                      160

Thr Val Tyr Gly Lys Thr Phe Asp Asp Cys Leu Glu Asn Leu Asp Lys
          165                      170                      175

Val Leu Gln Leu Cys Glu Gly Lys His Leu Ile Val Asn Glx Glu Lys
          180                      185                      190

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Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205

Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Thr Asn Val Lys Asp Ile Arg Ser Phe Leu Gly His  
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 130  
 <211> 761  
 <212> DNA  
 <213> Sorghum bicolor

<400> 130  
 gtgcgtaagg aggttttttaa gctgctgcat gcagagatta tatatcatgt gccgcacagt 60  
 gagtgggtaa gcccagttca agttgtgcct aaaaagggag gcatgattgt tgttacgaat 120  
 gaaaagaacg agctaattcc gcaacgcacc gtcacagggt ggcggatgtg catagactat 180  
 agaaaactaa acaaagccac gagaaaggat cattttcctt tacctttcat agatgagatg 240  
 ctagagcgat tagcaaacca ttcgttcttc tgtttcttag atggataatt agggatatcac 300  
 cagatcccaa tcaatcttga tgatcaaagc aaaccactt ttccatgcc acatggaact 360  
 tatgcttacc gtagaatgtc ttttgggtta tgtaatgcac cagcttcttt tcaaagatgc 420  
 atgatgtctg tattttctaa tatgattgaa gagattatgg aattttcatg gatgatttct 480  
 ctgtttatgg aaaaactttt gatagttgtc ttgaaaactt agacagggtt ttgcaaagat 540  
 gtgaagaaaa gtacttagtc ctttaattgga aaaaatgtca ttttatgggt aggggaaggaa 600  
 tagtgctggg acacctagtg tctgaaagag gtattgaggt cgacaaagct aaaattgaag 660  
 taattgaaca actacctcca cctttgaata taaaaggaat tcgaagcttt cttggccatg 720  
 ctgggttttta tcgtagattc attaaggact ttacaaagggt t 761

<210> 131  
 <211> 254  
 <212> PRT  
 <213> Sorghum bicolor

<400> 131  
 Val Arg Lys Glu Val Phe Lys Leu Leu His Ala Glu Ile Ile Tyr His  
 1 5 10 15  
 Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
 20 25 30  
 Gly Gly Met Ile Val Val Thr Asn Glu Lys Asn Glu Leu Ile Pro Gln  
 35 40 45  
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx  
 85 90 95



Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr  
 100 105 110  
 Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val  
 130 135 140  
 Phe Ser Asn Met Ile Glu Glu Ile Met Glu Ile Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys  
 180 185 190  
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser  
 195 200 205  
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln  
 210 215 220  
 Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 132  
 <211> 763  
 <212> DNA  
 <213> Sorghum bicolor

<400> 132  
 gtgcggaag aggtcgtcaa gctctatcat gctgggatta tttatcctgt gccacatagt 60  
 gagtgggtta gccctgttca agtagtgcca aagaaagaag gaatgacggt cgtaggaat 120  
 gagaagaatg aactcatccc tcaacaaatt gtcactagat ggcgatgtg tattgactat 180  
 cgaaaactca acaaaagctac aaagaaagat cactttccgt tacccttcat tgatgaaatg 240  
 ttggaatggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300  
 caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtattgaact 360  
 tatgcatact gacgaatgtc gttcggattg tgcaatgctc tagcttcttt tccagcgggtg 420  
 catgatgtct attttctcgg acatgattga gaagatcatg gaggttttca tggatgattt 480  
 taccgtctat ggcaaaacct tcgatcattg tttggagaat ttagatagag tcttgacgag 540  
 atgtgaggaa aatcacttaa tcttgaactg ggagaaatgt cattttatgg ttcaggaagg 600  
 aatagtgtta ggacataaag tgtccgaacg tggatatagat gtggacaaag caaagattaa 660  
 agttattgaa aaacttccac ctcacacgaa tgtgaaagga atccatagct ttttgggaca 720  
 tgcagggttc tatagacgct tcatcaagga tttcacaaag gtt 763

<210> 133  
 <211> 254  
 <212> PRT  
 <213> Sorghum bicolor

<400> 133

Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro  
1 5 10 15

Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln  
35 40 45

Gln Ile Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met  
65 70 75 80

Leu Glu Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Tyr Glx Thr Tyr Ala Tyr Glx Arg Met Ser Phe  
115 120 125

Gly Leu Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile  
130 135 140

Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg  
165 170 175

Val Leu Gln Arg Cys Glu Glu Asn His Leu Ile Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Glu Arg Gly Ile Asp Val Asp Lys Ala Lys Ile Lys Val Ile Glu Lys  
210 215 220

Leu Pro Pro His Thr Asn Val Lys Gly Ile His Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 134

<211> 756

<212> DNA

<213> Sorghum bicolor

<400> 134

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aaggagggttt tcaagttgct gcatgcaggg attatatatc ttgtgccgca tagtgagtgg 60
gtaagcccag ttcaagttgt gcctaaaaag ggaggcatga ctattattat gaatgaaaag 120
aacgagctaa ttccgcaacg caccgttaca gtatggcgga tgtgcataga ctatagaaaa 180
ctaaacaaaag ccacgagaga ggatcacttt cctttacctt tcatagatga gatgctagag 240
tggttagcaa accattcggt cttctgtttc ttagatggat attgagggta tcatcagatc 300
ccgatccatc ccgatgatca aagcaaaacc actttttacat gcccatatgg aacttatgct 360
taccgtagaa tgtcttttgg gttatgtaat gcactagctt cttttcaaag atgcatgatg 420
tctatatattt ctgatatgat tgaagagatt atggaagttt tcatggatga tttctctggt 480
tatggaaaaa cttttgatag ttgtcttaaa aacttagaca aggttttgca aagatgtgaa 540
gaaaagcact tagtccttaa ttgggaaaaa tgtcatttca tggttaggga aggaatagtg 600
ctgggacact tagtgtctga aagagctatt gaggtagata aagctaaaat tgaagtaatt 660
gaacaactac gtccacctgt gaacataaaa ggaatttgaa gctttcttgg ccatgctggt 720
tttcatcgta gattcataaa agactttaca aagggtt 756

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<210> 135  
 <211> 252  
 <212> PRT  
 <213> Sorghum bicolor

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<400> 135
Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro
  1             5             10             15

His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly
      20             25             30

Met Thr Ile Ile Met Asn Glu Lys Asn Glu Leu Ile Pro Gln Arg Thr
      35             40             45

Val Thr Val Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn Lys Ala
      50             55             60

Thr Arg Glu Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met Leu Glu
      65             70             75             80

Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr Glx Gly
      85             90             95

Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Ser Lys Thr Thr Phe
      100             105             110

Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe Gly Leu
      115             120             125

Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile Phe Ser
      130             135             140

Asp Met Ile Glu Glu Ile Met Glu Val Phe Met Asp Asp Phe Ser Val
      145             150             155             160

Tyr Gly Lys Thr Phe Asp Ser Cys Leu Lys Asn Leu Asp Lys Val Leu
      165             170             175

Gln Arg Cys Glu Glu Lys His Leu Val Leu Asn Trp Glu Lys Cys His
      180             185             190

```

Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser Glu Arg  
 195 200 205

Ala Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln Leu Arg  
 210 215 220

Pro Pro Val Asn Ile Lys Gly Ile Glx Ser Phe Leu Gly His Ala Gly  
 225 230 235 240

Phe His Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 136  
 <211> 762  
 <212> DNA  
 <213> Glycine max

<400> 136  
 gtgcgtaagg aggttgtcaa gcttttggag gttgggctca tatacctcat ctctgacagc 60  
 gcttgggtaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120  
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180  
 tgcaagtga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240  
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatatc aggatacaac 300  
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgcc ctttggcgtc 360  
 tttgcttaca gaaggatgtc attcagggtta tgtaacgcac cagccacatt tcagaggtgc 420  
 gtgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480  
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540  
 tgcgtataga ctaacttggg actaaattag gaaaaatgtc atttcatggt tcgagagggg 600  
 atagtgatgg accacaatat ctacgctaga gggattgagg ttgatcaggc aaagatagac 660  
 gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt cttagggcat 720  
 gcaggtttct acaggagggt tatcaaggac ttcaccaagg tt 762

<210> 137  
 <211> 254  
 <212> PRT  
 <213> Glycine max

<400> 137  
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu  
 1 5 10 15  
 Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys  
 20 25 30  
 Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr  
 35 40 45  
 Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn  
 50 55 60  
 Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met  
 100 105 110  
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile  
 130 135 140  
 Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe  
 145 150 155 160  
 Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
 165 170 175  
 Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys  
 180 185 190  
 Cys His Phe Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser  
 195 200 205  
 Ala Arg Gly Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 138  
 <211> 763  
 <212> DNA  
 <213> Glycine max

<400> 138  
 gtgcgtaagg aggtcttttaa gttcttggag gctgggctca tatatcccat ctctaatagc 60  
 acttaggttaa gccaggtaca ggtgggtccc aagaaagggtg gaatgacagt agtacagaat 120  
 gagaagaatg acttgatacc aacacgaact gtcactagct ggcgaaatag catcgattat 180  
 cgcaagctga atgaggccac ccggaaggac cacttccctc tacctttcat ggatcagatg 240  
 ttggagagac ttgcagggca ggcggtattat tgtttcttgg atggatactc gagatataat 300  
 cagattgcgg tggaccctag agaccaagag aagacgacct tcacatgccc tttttggcgt 360  
 ctttgcttac agaaggatgc cattcggggt atgtaatgca ccagccacat ttcagagggtg 420  
 catgctggcc attttttcag acatgggtga gaaaaatgc gaggtattca tggatgactt 480  
 ttcagttttt ggccctcat ttgacagttg tttgaggaac cttagatgg tacttttagag 540  
 gtgcgtagag actaatttag tgctgaactg ggagaagtgt cattttatgg ttcgagaggg 600  
 catagtcttg agccacaaga tctcagctag agggattgag gttgaccggg caaagataga 660  
 cgtcatagag aagctgccac caccattgaa tattaaagg gtcagaagtt tcttagggca 720  
 tgcaggattc tacaggagat tcataaagga ctttacaag gtt 763

<210> 139  
 <211> 254  
 <212> PRT  
 <213> Glycine max

<400> 139

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asn Ser Thr Glx Val Ser Pro Val Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Val Gln Asn Glu Lys Asn Asp Leu Ile Pro Thr  
35 40 45

Arg Thr Val Thr Ser Trp Arg Ile Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Arg Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Thr  
100 105 110

Thr Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
130 135 140

Phe Ser Asp Met Val Glu Lys Asn Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Gly Pro Ser Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
165 170 175

Val Leu Glx Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Lys Ile Ser  
195 200 205

Ala Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Leu Asn Ile Lys Gly Val Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 140

<211> 762

<212> DNA

<213> Glycine max

<400> 140

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gtgcgcaagg aggttttgaa gcttctagag gttgggctta tctaccccat ctccgacagc 60
gcttgggtaa gccagtcctt ggtggtgtcg aagaaagagg gcatgacagt cattcgaaat 120
gaaaagaatg acctgatacc aacacgaact gtcactagtt ggaaattatg catcgattac 180
cgcaagctca acgaagccac aaggaaagac catttccttc tacccttcat ggatcagatg 240
ttggagagac ttgcaggaca cgcttattat tgcttcttgg atgcatactt tggatataat 300
cagattgttg tagaccccaa ggatcaggag aagatggcct tcacatgccc ttttgggtgc 360
tttgccctata gacggattcc atttgggttg tgcaatgcac ctaccacatt ccaaagtgtg 420
atgttggcca tttttgcaga tatagtggag aaaagcatcg aagtattcat ggatgacttt 480
tcagtatttg tgccctcatt agaaagtgtt ttgaagaagt tggagatggg actacaaaga 540
tgcggtgaaa caaacttagt actaaattgg gagaagtgtc acttcatggg tcgagaaggc 600
atagtcttag gccataaaat ttcgaccga ggaattgagg tagacaaac aaagattgat 660
gtcattgaaa agttgccacc accatcaaat gttaaaggca tcaggagctt cctaggacaa 720
gccaggttct acagaagatt catcaaggac ttcacaaaag tt 762

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<210> 141
<211> 254
<212> PRT
<213> Glycine max

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<400> 141
Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
  1              5              10              15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Leu Val Val Ser Lys Lys
      20              25              30

Glu Gly Met Thr Val Ile Arg Asn Glu Lys Asn Asp Leu Ile Pro Thr
      35              40              45

Arg Thr Val Thr Ser Trp Lys Leu Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
      65              70              75              80

Leu Glu Arg Leu Ala Gly His Ala Tyr Tyr Cys Phe Leu Asp Ala Tyr
      85              90              95

Phe Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Met
      100             105             110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Ile Pro Phe
      115             120             125

Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Met Cys Met Leu Ala Ile
      130             135             140

Phe Ala Asp Ile Val Glu Lys Ser Ile Glu Val Phe Met Asp Asp Phe
      145             150             155             160

Ser Val Phe Val Pro Ser Leu Glu Ser Cys Leu Lys Lys Leu Glu Met
      165             170             175

Val Leu Gln Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
      180             185             190

```

Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205

Thr Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Ser Asn Val Lys Gly Ile Arg Ser Phe Leu Gly Gln  
 225 230 235 240

Ala Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 142  
 <211> 762  
 <212> DNA  
 <213> Glycine max

<400> 142  
 gtgcggaagg aggttattaa gttgctagag gcagggctca tttacctaata ctcagatagt 60  
 tcataggtta gtcctgttca tgttgctctg aaaaagggag gtatgacagt gataaagaat 120  
 gatagagatg agttaattcc tacaagaata gttactggat ggaggatggg tattgattac 180  
 aagaagctaa atgaagccac caggaaaagac cattacccgc tccccttcat ggatcaaatg 240  
 cttgagagac ttgcagggca atcttcctac tatttattag atggatactc gggctacaat 300  
 caaattgcag tggatcctca ggaccaagaa aagacagctt tcacatgtcc ttttggtgta 360  
 tttgcttatc gccgcattgc gttcgggttta tgtaatgccc caactacttt ccagagatgt 420  
 atgatggcaa tttttgctga catggtaaag aaatgtattg aagtttttat ggacgatttc 480  
 tctgtctttg gtgcattctt tgaaaattgc ctacgaaatt tagagaaagt gttacaacgc 540  
 tatgaagaat ctaatttggt gctcaactgg gaaaaatgtc actttatggt tcaagaaggt 600  
 atcatgctgg gacacaagat ttctagaaga ggaattaagg tggataaggc aaagattgag 660  
 gttattgata aacttccacc tctagttaat gtttagaggc tacgaagttt tttgggtcat 720  
 gctagattct atcgatgatt tatcaaggac ttcaccaaag tt 762

<210> 143  
 <211> 254  
 <212> PRT  
 <213> Glycine max

<400> 143  
 Val Arg Lys Glu Val Ile Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu  
 1 5 10 15  
 Ile Ser Asp Ser Ser Glx Val Ser Pro Val His Val Ala Leu Lys Lys  
 20 25 30  
 Gly Gly Met Thr Val Ile Lys Asn Asp Arg Asp Glu Leu Ile Pro Thr  
 35 40 45  
 Arg Ile Val Thr Gly Trp Arg Met Gly Ile Asp Tyr Lys Lys Leu Asn  
 50 55 60  
 Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly Gln Ser Ser Tyr Tyr Leu Leu Asp Gly Tyr  
 85 90 95



Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr  
 100 105 110  
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Met Ala Ile  
 130 135 140  
 Phe Ala Asp Met Val Lys Lys Cys Ile Glu Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Phe Gly Ala Ser Phe Glu Asn Cys Leu Ala Asn Leu Glu Lys  
 165 170 175  
 Val Leu Gln Arg Tyr Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser  
 195 200 205  
 Arg Arg Gly Ile Lys Val Asp Lys Ala Lys Ile Glu Val Ile Asp Lys  
 210 215 220  
 Leu Pro Pro Leu Val Asn Val Arg Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Arg Phe Tyr Arg Glx Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 144  
 <211> 761  
 <212> DNA  
 <213> Glycine max

<400> 144  
 gtgcggaagg aggtctttaa gttgctggaa gcaggcctta tttatcccat ttcggatagt 60  
 gcatgggtta gccctatgca agttgtccct aagaaaggag gtatgacagt cattaagaat 120  
 gataaagatg agttgatatc cacaaggacc gtcaccgggt ggagaatgtg cattgactat 180  
 cgaaagctga atgatgcacc cggaaggacc attatccact ccctttcatg ggccatatgc 240  
 ttgaaagact tgttgggcaa tcctattatt gttttctaga tggatattat gggtataatc 300  
 agattgttgt agatcccaaa gatcaagaga agacagcttt cacctaccct tttgggtgtat 360  
 tcgcatatca gtgcatgcct tttggtctat gcaatgcccc agctacattt cagaggtgta 420  
 tgatggctat tttttctgat atggtggaaa tatgcattga agttttcatg gacgatttct 480  
 ctatttttgg gccatccttt gaagggtgct tatcaaactt tgaaaaagta ttaaagagat 540  
 gtgaagagtc caatctagtt ctcaattgga agaaatgcca tttcatgggt caagaaggaa 600  
 taatgttggg gcataaaaatt tcagtaagag gtagagaggt ggacaaggca aagattgatg 660  
 taattgagaa actacttgct cccatgaatg tcaagggaat aagaagcttc ttaggacatg 720  
 cagggttcta caggcgattc ataaaagact tcaccaaagt t 761

<210> 145  
 <211> 254  
 <212> PRT  
 <213> Glycine max

<400> 145

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr  
35 40 45

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
50 55 60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met  
65 70 75 80

Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr  
100 105 110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile  
130 135 140

Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys  
165 170 175

Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys  
180 185 190

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser  
195 200 205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
210 215 220

Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
245 250

<210> 146

<211> 762

<212> DNA

<213> Glycine max

<400> 146

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gtgcgtaagg aggtgggtcaa gttgcttgaa gtaggactaa tttatccaat ctctgatagt 60
gcttgggtga gttcgaacta ggtgggtgcct aagaaagggtg gtatgacggt gatccacaat 120
gataagaatg atcttattcc tacacagaca atcattaggt ggcaaattgtg tattgactat 180
cacaagttga atgatgtcac caagaaggac cattttcctc tgccattcat ggaccaaattg 240
ttagagaggt tagctggcca agctttttat tgttttttgg atgggttattc tgggtataac 300
caaatagcgg tgcatcttaa agatcaagag aagactacta tcatatgccc atttggtgtc 360
tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420
atgatggcca tttttgctga ccttggtggag aaatgcatag aggtgttcat gaatgatttc 480
tctattttcg gctcttcctt ttatcattgt ttatccaacc tggaattagt gttacaacgg 540
tgtgcggaaa ccaatttggt gatgaactgg gagaaatgtc atttcatggt ccaagagggg 600
attgtcttag gccacaagat ctcttcagga gggttggaag tggacaaggc aaaaattgat 660
gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720
gttggttttt ataggagggt catcaaagac ttcacgaaag tt 762

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<210> 147

<211> 254

<212> PRT

<213> Glycine max

<400> 147

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Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
  1                      5                      10                      15

```

```

Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys
          20                      25                      30

```

```

Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr
          35                      40                      45

```

```

Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn
          50                      55                      60

```

```

Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
          65                      70                      75                      80

```

```

Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
          85                      90                      95

```

```

Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr
          100                      105                      110

```

```

Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe
          115                      120                      125

```

```

Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile
          130                      135                      140

```

```

Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe
          145                      150                      155                      160

```

```

Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu
          165                      170                      175

```

```

Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys
          180                      185                      190

```

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205

Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr  
 225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 148

<211> 762

<212> DNA

<213> Glycine max

<400> 148

gtgcgtaagg aggttctcaa gcttttggag gttgggctca tatacctcat ctctgacagc 60  
 gcttgggttaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120  
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180  
 tgcaagttga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240  
 ctggagagggc ttgcagggca ggcatactac tgtttcttgg atagatatc aggatacaac 300  
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgcc ctttggcgctc 360  
 tttgcttaca gaaggatgtc attcagggtta tgtaacgcac cagccacatt tcagaggtgc 420  
 atgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480  
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540  
 tgcgtataga ctaacttggt actaaattag gaaaaatgtc atttcatggt tcgagagggg 600  
 atagtgatgg gccacaatat ctcagctaga gggattgagg ttgatcagac aaagatagac 660  
 gtcattgaga agttgccacc accactgaat gttaaaggcg tcagaagttt cttagggcat 720  
 gcaggtttct acaggagggt cataaaagac ttcacaaagg tt 762

<210> 149

<211> 254

<212> PRT

<213> Glycine max

<400> 149

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu  
 1 5 10 15

Ile Ser Asp Ser Ala Trp Val Ser Leu Val Gln Val Ala Pro Lys Lys  
 20 25 30

Cys Gly Met Thr Val Val Gln Asn Glu Arg Asn Asp Leu Ile Pro Thr  
 35 40 45

Arg Thr Val Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn  
 50 55 60

Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
 65 70 75 80

Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met  
 100 105 110  
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe  
 115 120 125  
 Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile  
 130 135 140  
 Phe Ser Asp Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe  
 145 150 155 160  
 Ser Ile Phe Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met  
 165 170 175  
 Val Leu Gln Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys  
 180 185 190  
 Cys His Phe Met Val Arg Glu Gly Ile Val Met Gly His Asn Ile Ser  
 195 200 205  
 Ala Arg Gly Ile Glu Val Asp Gln Thr Lys Ile Asp Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 150  
 <211> 761  
 <212> DNA  
 <213> Glycine max

<400> 150  
 gtgcgtaagg aggttttttaa gttgctggaa gcaggctcta tttatcccat ttcggatagt 60  
 gcatgggtta gccctgtgca ggtgtgtccc aagaaagaag gtaagacagt cattaaggat 120  
 gaaaaggatg agttgatatc cacaaggact atcaccgggt ggagaatgtg cattgactat 180  
 cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240  
 cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tggttataat 300  
 cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttggtgta 360  
 ttcgcctatc ggcgcatgcc ctttggtttg tgcaatgccc cagctacatt tcagaggtgt 420  
 atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatttc 480  
 tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540  
 cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600  
 atagtgtggg gcataaaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660  
 taatagagaa actacctcct cccatgaatg tcaagggaat aagaagcttc ctaggacatg 720  
 caggggttcta caagcgattc atcaaagatt tcacaaaggt t 761

<210> 151  
 <211> 254  
 <212> PRT  
 <213> Glycine max

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<400> 151
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
  1           5           10           15

Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20           25           30

Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
      35           40           45

Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
      50           55           60

Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
      65           70           75           80

Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85           90           95

Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
      100          105          110

Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115          120          125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
      130          135          140

Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe
      145          150          155          160

Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
      165          170          175

Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
      180          185          190

Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
      195          200          205

Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
      210          215          220

Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
      225          230          235          240

Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
      245          250

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<210> 152
<211> 762
<212> DNA
<213> Glycine max

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<400> 152

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gtgcggaaaag aggtattcaa gttactagag gcagggctca tctacccaat ttcagatagc 60
tcctgggtta gtccggttca agttgttcca aaaaaaggag ggatgacagt ggtaaaaaat 120
gatagaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180
aggaagctca atgaagccac aagaaaagac cattaccac ttcccttcat ggatcaaatg 240
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggatactc aggttacaat 300
cagattgcag tggatcctca ggatcaagaa aaaacagctt ttacatgtcc tttcagtgtt 360
tttgcttata gccgcatgcc gttcggttta tgtaatgcct ctactacttt tcagagatgt 420
atgatggcaa tttttgatga catggtagag aaatgtattg aagtctttat ggatgatttt 480
tcgttctttg gtgcatcttt tggaaattgc ttagcaaatt tagagaaaagt gttacaacgt 540
tgtgaaaaat ctaattttgg gcttaactgg gaaaaatgtc actttatggg acaagaaggt 600
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggttaaaga aaaactagat 660
gttattgata aacttccacc cccagttaat gtaaaaggca tacacagttt tttgggtcat 720
gttggatttt atcggcgatt cataaaggac ttcaccaaag tt 762

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<210> 153

<211> 254

<212> PRT

<213> Glycine max

<400> 153

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Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
  1                      5                      10                      15

Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20                      25                      30

Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr
      35                      40                      45

Arg Arg Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
      50                      55                      60

Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
      65                      70                      75                      80

Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr
      85                      90                      95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
      100                      105                      110

Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe
      115                      120                      125

Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile
      130                      135                      140

Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe
      145                      150                      155                      160

Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys
      165                      170                      175

Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys
      180                      185                      190

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Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205

Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys  
 210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His  
 225 230 235 240

Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 154  
 <211> 761  
 <212> DNA  
 <213> Glycine max

<400> 154  
 gtgcgtaaaag aagtttttgaa gctgctagaa gcagacctta tttatcccat ttcggatagt 60  
 acatgggtta gccctgtgca agttgtcccc gagaaaggag gtatgacagt cattaagaat 120  
 gataaagatg agttgatatc cacaaggact gtcaccgggt gagaatgtgc attgactatc 180  
 ggaagctgaa tgatgccacc cagaaggacc attattcact ccctttcatg gaccagatgc 240  
 ttgaaagact tgccggacaa tcctattatt gttttctgaa tggatactct ggctataatc 300  
 agattgtggt agatcccaaa gatcaggaga aaactgcttt cacctgcctt tttggtgtat 360  
 ttgcatacaa gcgtatgcat tttggcttgt gtaatgctcc aactacgtgt cagaggtgta 420  
 tgatgactat tttttctggt atcgtggaaa aatgcattga acttttcatg gacgatttct 480  
 ctattttttg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540  
 gtgaagagtc taatctagtt ctcaattggg agaaatgcca tttcatggtt caagaaggaa 600  
 tagtgctggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660  
 taattgagaa actacctcct cccatgattg tcaagggaat aagaagcctc ctaggacatg 720  
 tagggttcta caggcgattc atcaaagact tcacaaagggt t 761

<210> 155  
 <211> 254  
 <212> PRT  
 <213> Glycine max

<400> 155  
 Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro  
 1 5 10 15  
 Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys  
 20 25 30  
 Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr  
 35 40 45  
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn  
 50 55 60  
 Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr  
 85 90 95



Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr  
 100 105 110  
 Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile  
 130 135 140  
 Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg  
 165 170 175  
 Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His  
 225 230 235 240  
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

gtgcgtaagg aggttttttaa gttgctggaa gcaggctcta tttatcccat ttcggatagt 60  
 gcatgggtta gccctgtgca ggttgctccc aagaaagaag gtaagacagt cattaaggat 120  
 gaaaaagatg agttgatatc cacaaggact atcaccgggt ggagaatgtg cattgactat 180  
 cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagt 240  
 cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tgggtataat 300  
 cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttggtgta 360  
 ttcgcctatc ggcgcatgcc ctttggtttg tgcaatgccc cagctacatt tcagagggtg 420  
 atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatgtc 480  
 tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540  
 cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600  
 atagtgttgg ggcataaaat ttcagtaaga gggatagagg tggacaaggc aaagattgat 660  
 gtaatagaga aactacctcc tcccatgaat gtcaagggaa taagaagctt cctaggacat 720  
 gcagggttct acaagcgatt catcaaagac ttctcaaaag tt 762

<210> 157

<211> 254

<212> PRT

<213> Glycine max

<400> 157  
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro  
 1 5 10 15  
 Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys  
 20 25 30  
 Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr  
 35 40 45  
 Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn  
 50 55 60  
 Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95  
 Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr  
 100 105 110  
 Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile  
 130 135 140  
 Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val  
 145 150 155 160  
 Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg  
 165 170 175  
 Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220  
 Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val  
 245 250

<210> 158  
 <211> 761  
 <212> DNA  
 <213> Glycine max

<400> 158

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gtgcggaagg aggttcttaa gtcctggaa gcagggctca tctatcttat ctcagatagt 60
gttgggtgag tccagtgcac gtggttccca agaagggtgg gaagactgtg gtgagaaatg 120
agaaaaatga cctcattcta acccgaactg tcacaggatg gagaatgtgc atagattatc 180
ggaagttgaa tgatgccatc aagaaggatc acttcctct accattcata gatcagatgc 240
ttgagagggtt agcaagccag tctttctatt atttcttggg tgaatattct agatacaatc 300
agattgctat acatcccaag gaccaagaga agattgcatt tacatgcca tttggtgtct 360
ttgcctatag aaggatgcca tttgaactat gcaatgctcc agctaccttt tagaggcata 420
tgctagccat attcgctaac atgggtggaga aatgcacgca agtggtcata gatgattttt 480
cgggtgtttgg tccatccttt gtttgttggt tgaccaattt agagctagtgt ttgaagtact 540
gtgaggagac aaatttagta ttgaattggg agaaatgtca tttcatgggc caagaaggaa 600
ttatgttggg gcataaaatt tttgctagag gtattgaggt ggacaaggcc aaaattgatg 660
ttattgaaaa gctgcctcca ccagtcaatg taaaaggcat caggagtttt cttggacaca 720
ctggtttctt caggcgtttc atcaaggact tcacaaaagt t 761

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<210> 159

<211> 254

<212> PRT

<213> Glycine max

<400> 159

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Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu
  1              5              10              15

```

```

Ile Ser Asp Ser Ala Trp Val Ser Pro Val His Val Val Pro Lys Lys
      20              25              30

```

```

Gly Gly Lys Thr Val Val Arg Asn Glu Lys Asn Asp Leu Ile Leu Thr
      35              40              45

```

```

Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
      50              55              60

```

```

Asp Ala Ile Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
      65              70              75              80

```

```

Leu Glu Arg Leu Ala Ser Gln Ser Phe Tyr Tyr Phe Leu Asp Glu Tyr
      85              90              95

```

```

Ser Arg Tyr Asn Gln Ile Ala Ile His Pro Lys Asp Gln Glu Lys Ile
      100             105             110

```

```

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115             120             125

```

```

Glu Leu Cys Asn Ala Pro Ala Thr Phe Glx Arg His Met Leu Ala Ile
      130             135             140

```

```

Phe Ala Asn Met Val Glu Lys Cys Ile Glu Val Phe Ile Asp Asp Phe
      145             150             155             160

```

```

Ser Val Phe Gly Pro Ser Phe Val Cys Cys Leu Thr Asn Leu Glu Leu
      165             170             175

```

```

Val Leu Lys Tyr Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
      180             185             190

```

Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Phe  
 195 200 205

Ala Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240

Thr Gly Phe Phe Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 160  
 <211> 762  
 <212> DNA  
 <213> Pisum sativum

<400> 160  
 gtgcgcaagg aagtactcaa gttgttagat tcgggaatga tttaccccat ttctgacagc 60  
 tcgtgggttaa gtccagtgcg cgtgggtacca aagaaaggag gaacctcagt aatttttaa 120  
 gaaaagaatg aactgatccc aactcgcaca gtgacagggt ggcgagtatg catcgatcac 180  
 agaagactga acacagcaac aagaaaggat cattttcctc tcccttttat tgatcaaatg 240  
 ttagaaagac ttgcagggtca tgagtattat tgctttctgg atggatattc gggatacaat 300  
 caaattgttg tagccccgga agatcaggaa aaaactgcat ttacatgtcc ttatggtatt 360  
 ttcgcttaca gacggatgcc atttgggcta tgcaatgccc cagctacttt tcagaggtgt 420  
 atgacatcta tattctccga catgcttgaa aagtatatga aggtgtttat ggatgatttc 480  
 tctgtgtttg gttcttcttt tgataattgt ttagctaact tgtctcttgt ttgcaaaga 540  
 tgtcaggaaa ctaaccttgt tctcaattgg gagaaatgtc atttcatggt gcaggaagga 600  
 attgtgctag gacacaaaat ttcccacaaa ggaattgaag tggacaaagc caaagtggag 660  
 gttatagcta acctcccacc tccggtgaat gaaaaaggga taaggagttt tttgggtcat 720  
 gcagggtttt atcgcagggt catcaaagac ttcacaaagg tt 762

<210> 161  
 <211> 254  
 <212> PRT  
 <213> Pisum sativum

<400> 161  
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ser Gly Met Ile Tyr Pro  
 1 5 10 15  
 Ile Ser Asp Ser Ser Trp Val Ser Pro Val His Val Val Pro Lys Lys  
 20 25 30  
 Gly Gly Thr Ser Val Ile Leu Asn Glu Lys Asn Glu Leu Ile Pro Thr  
 35 40 45  
 Arg Thr Val Thr Gly Trp Arg Val Cys Ile Asp His Arg Arg Leu Asn  
 50 55 60  
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met  
 65 70 75 80  
 Leu Glu Arg Leu Ala Gly His Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Val Val Ala Pro Glu Asp Gln Glu Lys Thr  
 100 105 110  
 Ala Phe Thr Cys Pro Tyr Gly Ile Phe Ala Tyr Arg Arg Met Pro Phe  
 115 120 125  
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Thr Ser Ile  
 130 135 140  
 Phe Ser Asp Met Leu Glu Lys Tyr Met Lys Val Phe Met Asp Asp Phe  
 145 150 155 160  
 Ser Val Phe Gly Ser Ser Phe Asp Asn Cys Leu Ala Asn Leu Ser Leu  
 165 170 175  
 Val Leu Gln Arg Cys Gln Glu Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190  
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser  
 195 200 205  
 His Lys Gly Ile Glu Val Asp Lys Ala Lys Val Glu Val Ile Ala Asn  
 210 215 220  
 Leu Pro Pro Pro Val Asn Glu Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240  
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 162  
 <211> 762  
 <212> DNA  
 <213> Pisum sativum

<400> 162  
 gtgcgtaagg aggtctttaa actattggat gcgggaatga tttacccgat ctcgatagat 60  
 ccgtgggtta gtcccgtgca cgtgggtccg aagaaggggtg gaatgaccgt aatccgtaat 120  
 gacaaagacg aattgatccc gactaaagt gcaacgggggt ggagaatatg tatagattat 180  
 agacagttga ataccgcgac tcgaaaggac cattttccac tcccatttat ggatcaaatg 240  
 cttgaaagac tatcgggcca acaatactat tgtttcttgg acggctactc cgggtacaac 300  
 caaattgcgg ttgacccgggt tgatcatgag aagacggctt tcacgtgtcc gtttggagtg 360  
 ttcgcataca gaaaaatgcc ctttgggctg tgcaatgcac cggcgacttt ccaacgatgc 420  
 gtcctagcca tttttgccga tctaataagag aaaacaatgg acgtcttcat ggatgacttc 480  
 tcggtatttg gtgggacggt tagtctatgc ttggcaaatt tgaagacggt gttggaaagg 540  
 tgtgtgaaga ccaatttgggt gctaaattgg gaaaagtgtc acttcatggt gaccgagggg 600  
 atcgtgctag gccacaaagt ctctaaaagg gggccttgaag tggatagagc taagggttgaa 660  
 gtaattgaaa aattaccccc tccggtgaat tgaaaaggca tccgtagctt tttggggcac 720  
 gcgggggttt accggcgctt cattaaagac ttctcaaaag tt 762

<210> 163  
 <211> 254  
 <212> PRT  
 <213> Pisum sativum

<400> 163

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro  
1 5 10 15

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys  
20 25 30

Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr  
35 40 45

Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn  
50 55 60

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
65 70 75 80

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr  
85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr  
100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe  
115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile  
130 135 140

Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe  
145 150 155 160

Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr  
165 170 175

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys  
180 185 190

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser  
195 200 205

Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val  
245 250

<210> 164

<211> 762

<212> DNA

<213> Pisum sativum

<400> 164

gtgcggaagg aggtctttaa attgttggat gcgggggatga tttacccgat ctcggatagt 60  
 ccatgggtta gtcctgtgca cgttgttccg aagaaggggg ggattaccgt aatccggaat 120  
 gacaaggatg aattgatccc cactaaagtt gaaacggggg ggagaatgtg tattgattat 180  
 aggcgggttg ataccgcgac tcgaaaagac cattttccac tcccatttat ggatcaaatg 240  
 ctcgaaagac tatcggggcca acaatattat tgtttttttg acggctactc cgggtacaac 300  
 caaattgcgg ttgaccgggc cgatcatgag aagacgggctt tcacatgtcc gtttggagtg 360  
 ttgcgatacc gaaaaatgcc ctttggggctg tgcaatgcac cggcgacctt ccaacgatgt 420  
 gtccaagcca tttttgtcga tctgatagag aaaacaatgg aagtcttcat ggatgacttc 480  
 tcggtatttg gtgggtcttt tagtctatgc ttggcgaaact tgaaaacggg gttggagaga 540  
 tgtgtgaaga ccaatttggg gcttaattgg gagaagtgtc acttcatggg gaccgagggg 600  
 atcgtgctag gccacaaagt ctctagaagg gggcttgaag tggaatagagc taagggtgaa 660  
 gtgatagaaa aattacctcc tccggtgaat gtgaagggca tccgaagctt tttggggcac 720  
 gccgggttct accggcgctt cattaaagat ttcacaaagg tt 762

<210> 165

<211> 254

<212> PRT

<213> Pisum sativum

<400> 165

Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro  
 1 5 10 15

Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys  
 20 25 30

Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr  
 35 40 45

Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn  
 50 55 60

Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met  
 65 70 75 80

Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr  
 85 90 95

Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr  
 100 105 110

Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe  
 115 120 125

Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile  
 130 135 140

Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe  
 145 150 155 160

Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr  
 165 170 175

Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys  
 180 185 190

Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser  
 195 200 205

Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys  
 210 215 220

Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His  
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val  
 245 250

<210> 166  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetically generated

<221> misc\_feature  
 <222> 6, 15, 16, 18  
 <223> n = A,T,C or G

<400> 166  
 gtgcgnaarg argtnntnaa ryt

23

<210> 167  
 <211> 8  
 <212> PRT  
 <213> Consensus sequence

<400> 167  
 Val Arg Lys Glu Val Leu Lys Leu  
 1 5

<210> 168  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetically generated

<221> misc\_feature  
 <222> 7  
 <223> n = A,T,C or G

<400> 168  
 aacyttngwr aartcyttta traa

24

<210> 169  
 <211> 8  
 <212> PRT  
 <213> Consensus sequence

<400> 169



Val Lys Ser Phe Asp Lys Ile Phe  
1 5

<210> 170  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 170  
gggatccgca attagaatct 20

<210> 171  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 171  
cgaattcggc ccacttcgga 20

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 172  
ccacaagatt ctaattgcgg attc 24

<210> 173  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 173  
ccgaaatgga ccgaacccga catc 24

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 174

tttccaggct cttgacgaga tttg 24

<210> 175  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 175  
 cgactcgagc tccatagcga tg 22

<210> 176  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 176  
 cggattgggc cgaaatggac cgaa 24

<210> 177  
 <211> 18  
 <212> DNA  
 <213> Arabidopsis thaliana

<400> 177  
 gaggacttgg ggggcaaa 18

<210> 178  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<221> VARIANT  
 <222> 2, 3, 5, 6, 7, 9, 10, 11, 12  
 <223> Any amino acid

<400> 178  
 Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys  
 1 5 10

<210> 179  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<400> 179

Leu Ile Glu Leu Gly Ala  
1 5

<210> 180  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<400> 180  
Lys Thr Ala Phe  
1

<210> 181  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
<222> 2  
<223> Pro or Ser

<400> 181  
Met Xaa Ser Phe Gly Leu Cys Asn Ala  
1 5

<210> 182  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
<222> 1  
<223> Val, Ile, or Met

<221> VARIANT  
<222> 9  
<223> Ser or Trp

<221> VARIANT  
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<223> Val or Ile

<400> 182  
Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa  
1 5 10

<210> 183  
<211> 19

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
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<223> Ile or Val

<400> 183  
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Gly Gln Arg

<210> 184  
<211> 27  
<212> PRT  
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<220>  
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<221> VARIANT  
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<223> Thr or Ile

<221> VARIANT  
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<223> Leu or Met

<221> VARIANT  
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<223> Phe or Tyr

<221> VARIANT  
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<221> VARIANT  
<222> 19  
<223> Arg or Lys

<221> VARIANT  
<222> 23  
<223> Ile or Val

<221> VARIANT  
<222> 26  
<223> Arg or Lys

<400> 184  
Tyr Ala Thr Xaa Glu Lys Glu Xaa Leu Ala Ile Val Xaa Ala Xaa Glu  
1 5 10 15  
Lys Phe Xaa Ser Tyr Leu Xaa Gly Ser Xaa Val  
20 25

<210> 185  
 <211> 46  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<221> VARIANT  
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 <223> Any amino acid

<400> 185  
 His Cys His Xaa Ser Xaa Xaa Gly Gly His Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Asp Xaa Cys Gln Arg  
 35 40 45

<210> 186  
 <211> 8  
 <212> PRT  
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<220>  
 <223> Consensus sequence

<221> VARIANT  
 <222> 6  
 <223> Ile, Val or Met

<400> 186  
 Trp Gly Ile Asp Phe Xaa Gly Pro  
 1 5

<210> 187  
 <211> 11  
 <212> PRT  
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<220>  
 <223> Consensus sequence

<221> VARIANT  
 <222> 7  
 <223> Any amino acid

<221> VARIANT  
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 <223> Ala or Val

<400> 187  
 Phe Tyr His Pro Gln Thr Xaa Gly Gln Xaa Glu  
 1 5 10

<210> 188  
<211> 13  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> misc\_feature  
<222> 11, 12  
<223> n = A, T, C or G

<400> 188  
atttggggra nnt

13

<210> 189  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
<222> 5, 8  
<223> Arg or Lys

<400> 189  
Gln Met Ala Ser Xaa Lys Arg Xaa Ala  
1 5

<210> 190  
<211> 6  
<212> PRT  
<213> Pisum sativum

<400> 190  
Ala Ser Lys Lys Arg Lys  
1 5

*By hand  
conserved  
CI  
conserved*